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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.

DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

5

TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, eukaryotic cells
10 expressing these DNAs and antibodies directed to these proteins. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies directed to these proteins. The human cDNAs of the present invention can be utilized as probes for genetic
15 diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for producing the proteins encoded by these cDNAs in large quantities. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantities can be
20 utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibodies of the present invention can be utilized for the detection, quantification, purification and the like of the proteins of the present invention.

25

BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like are currently employed as pharmaceuticals. In addition, secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is expected to lead to development of novel pharmaceuticals utilizing them.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like in the material transport and the signal transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion

channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides and amino acids and the like. The genes for many of them have already been cloned. It has been clarified that abnormalities in these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, so that isolation of new genes encoding the membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

In general, a secretory protein or a membrane protein possesses at least one hydrophobic domain within the protein. After synthesis on ribosomes, such domain works as a secretory signal or remains in the phospholipid membrane to be entrapped in the membrane. Accordingly, if the existence of a highly hydrophobic domain is observed in the amino acid sequence of a protein encoded by a cDNA when the

whole base sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

5 OBJECTS OF INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells that are capable of
10 expressing these DNAs and antibodies directed to these proteins. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

15

SUMMARY OF INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA
20 bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and
25 121 to 130. Moreover, the present invention provides a DNA

encoding said protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150, an expression vector that is capable of expressing
5 said DNA by in vitro translation or in eukaryotic cells, a transformed eukaryotic cell that is capable of expressing said DNA and of producing said protein and an antibody directed to said protein.

10 BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03171.

Fig. 2 illustrates the
15 hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03424.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03444.

20 Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03478.

Fig. 5 illustrates the
25 hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03499.

Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03500.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10691.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10703.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10711.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10712.

Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03010.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03576.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03611.

Fig. 14 illustrates the

hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03612.

Fig. 15 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
5 by clone HP10407.

Fig. 16 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10713.

Fig. 17 illustrates the
10 hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10714.

Fig. 18 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10716.

Fig. 19 illustrates the
15 hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10717.

Fig. 20 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
20 by clone HP10718.

Fig. 21 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03745.

Fig. 22 illustrates the
25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP03747.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10719.

5 Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10720.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
10 by clone HP10721.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10725.

Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
15 by clone HP10727.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10728.

20 Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10730.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
25 by clone HP10742.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03800.

Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03831.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03879.

10 Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03880.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10704.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10715.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10724.

Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10733.

25 Fig. 39 illustrates the

hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10734.

Fig. 40 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
5 by clone HP10756.

Fig. 41 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03670.

Fig. 42 illustrates the
10 hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03688.

Fig. 43 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03825

15 Fig. 44 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03877.

Fig. 45 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
20 by clone HP10765.

Fig. 46 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10766.

Fig. 47 illustrates the
25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP10770.

Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10772.

5 Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10773.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
10 by clone HP10776.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins
15 from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequences of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the
20 present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the cDNA of the present invention, and then
25 carrying out in vitro translation using this RNA as a

template. Alternatively, incorporation of the translated region into a suitable expression vector by the method known in the art may lead to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eukaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by incorporating the translated region of this cDNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing promoters for these RNA polymerases are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant

expression vector in which the translated region of the cDNA of the present invention is incorporated into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator and the like is constructed. After transformation of the host cells with this expression vector, the resulting transformant is cultivated, whereby the protein encoded by the cDNA can be produced in large quantities in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region to express the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the surface of cell membrane, by incorporating the translated region of the cDNA into an expression vector for eukaryotic

cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, 5 pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells, Chinese hamster ovary CHO cells and the like, budding yeasts, fission yeasts, silkworm cells, *Xenopus* oocytes and the like. 10 Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method known in the art such as the electroporation method, the calcium phosphate method, the 15 liposome method, the DEAE-dextran method and the like.

After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated and purified from the culture by a combination of separation procedures known in 20 the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric 25 focusing, ion-exchange chromatography, hydrophobic

chromatography, affinity chromatography, reverse phase chromatography and the like.

The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP-A 8-187100]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are added. Accordingly, such proteins or peptides to which sugar chains are added shall also come

within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a
5 method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)⁺ RNAs extracted from human cells as templates. The human cells may
10 be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and
15 Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can
20 be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for
25 colony or plaque hybridization according to a method known

in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest
5 are synthesized, which oligonucleotides are then used as the primers.

The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71
10 to 80, 101 to 110 and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Tables 1 and 2 summarizes the clone number (HP number), the cell from which the cDNA clone was obtained, the total number of bases of the cDNA, and the
15 number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID NO.	HP number	Cell	Number of bases	Number of amino acid residues
1, 11, 21	HP03171	Thymus	2042	267
2, 12, 22	HP03424	Liver	1433	419
3, 13, 23	HP03444	Kidney	1917	415
4, 14, 24	HP03478	Umbilical cord blood	2258	380
5, 15, 25	HP03499	Kidney	1973	585
6, 16, 26	HP03500	kidney	1606	331
7, 17, 27	HP10691	Umbilical cord blood	2380	345
8, 18, 28	HP10703	Kidney	2017	89
9, 19, 29	HP10711	Kidney	1606	406
10, 20, 30	HP10712	Kidney	1695	192
31, 41, 51	HP03010	Kidney	1551	377
32, 42, 52	HP03576	Kidney	1713	81
33, 43, 53	HP03611	Kidney	1758	487
34, 44, 54	HP03612	Kidney	1550	375
35, 45, 55	HP10407	Stomach cancer	1485	350
36, 46, 56	HP10713	Kidney	2694	667
37, 47, 57	HP10714	Umbilical cord blood	3297	464
38, 48, 58	HP10716	Umbilical cord blood	2126	470
39, 49, 59	HP10717	Kidney	1781	243
40, 50, 60	HP10718	Umbilical cord blood	1788	270
61, 71, 81	HP03745	Kidney	1376	389
62, 72, 82	HP03747	Umbilical cord blood	2392	348
63, 73, 83	HP10719	Kidney	1416	261
64, 74, 84	HP10720	Kidney	1347	222
65, 75, 85	HP10721	Kidney	2284	183

Table 2

SEQ ID NO	HP number	Cell	Number of bases	Number of amino acid residues
66, 76, 86	HP10725	Kidney	1737	262
67, 77, 87	HP10727	Umbilical cord blood	1556	168
68, 78, 88	HP10728	Umbilical cord blood	1855	243
69, 79, 89	HP10730	Umbilical cord blood	2530	428
70, 80, 90	HP10742	Umbilical cord blood	1911	283
91, 101, 111	HP03800	Umbilical cord blood	1633	476
92, 102, 112	HP03831	Kidney	1095	226
93, 103, 113	HP03879	Kidney	1602	305
94, 104, 114	HP03880	Kidney	897	227
95, 105, 115	HP10704	Kidney	1866	441
96, 106, 116	HP10715	Umbilical cord blood	2198	265
97, 107, 117	HP10724	Umbilical cord blood	2180	208
98, 108, 118	HP10733	Umbilical cord blood	1527	400
99, 109, 119	HP10734	Umbilical cord blood	1905	192
100, 110, 120	HP10756	Kidney	998	260
121, 131, 141	HP03670	Umbilical cord blood	1622	337
122, 132, 142	HP03688	Umbilical cord blood	2475	236
123, 133, 143	HP03825	Kidney	1739	560
124, 134, 144	HP03877	Kidney	2005	406
125, 135, 145	HP10765	Umbilical cord blood	1558	453
126, 136, 146	HP10766	Kidney	1005	59
127, 137, 147	HP10770	Kidney	969	210
128, 138, 148	HP10772	Kidney	1241	165
129, 139, 149	HP10773	Kidney	1174	162
130, 140, 150	HP10776	Kidney	1012	221

The same clones as the cDNAs of the present invention can be easily obtained by screening the cDNA

5 libraries constructed from the human cell lines or human

tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150.

5 In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131
10 to 150 shall come within the scope of the present invention.

 Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come within the scope of the present invention, as long as
15 the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

 The cDNAs of the present invention also include cDNA fragments (of 10 bp or more) containing any partial
20 base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Also, DNA fragments consisting of a sense strand and an anti-sense
25 strand shall come within this scope. These DNA fragments can

be utilized as the probes for the genetic diagnosis.

The antibody of the present invention can be obtained from a serum after immunizing an animal using the protein of the present invention as an antigen. A peptide
5 that is chemically synthesized based on the amino acid sequence of the present invention and a protein expressed in eukaryotic or prokaryotic cells can be used as an antigen. Alternatively, an antibody can be prepared by introducing the above-mentioned expression vector for eukaryotic cells
10 into the muscle or the skin of an animal by injection or by using a gene gun and then collecting a serum therefrom (JP-A 7-313187). Animals that can be used include a mouse, a rat, a rabbit, a goat, a chicken and the like. A monoclonal antibody directed to the protein of the present invention
15 can be produced by fusing B cells collected from the spleen of the immunized animal with myelomas to generate hybridomas.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological
20 activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as,
25 for example, in gene therapies or vectors suitable for

introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein

(such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell '75:791-803 (1993)) to identify polynucleotides
5 encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-
10 throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding
15 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for
20 example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or
25 agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation

Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol.

145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

5 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan
10 eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

15 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology.
20 J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-
25 Nordan, R. In Current Protocols in Immunology. J.E.e.a.

Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In
5 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John
10 Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include,
15 without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines
20 and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

25 Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune

pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by

the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant.

Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate

activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy.

Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function
5 may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be
10 enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing
15 the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a
20 portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or
25 enhancement of antigen function (preferably B lymphocyte

antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a

cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E.

Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies
5 in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic
10 cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of
15 Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and
20 Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate
25 lymphocyte homeostasis) include, without limitation, those

described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 5 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without 10 limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

15 A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates 20 involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to 25 stimulate the production of erythroid precursors and/or

erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and

differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without
5 limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

10 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I.
15 Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I.
20 Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New
25 York, NY. 1994; Long term bone marrow cultures in the

presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth

repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful
5 in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue
15 is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to
20 tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the
25 repair of congenital, trauma induced, or other tendon or

ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming
5 cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be
10 useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be
15 useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to
20 neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's,
25 Parkinson's disease, Huntington's disease, amyotrophic

lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and
5 cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to
10 promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

It is expected that a protein of the present
15 invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for
20 promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

25 A protein of the present invention may also be

useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

5 A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

 The activity of a protein of the invention may,
10 among other means, be measured by the following methods:

 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve,
15 neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year
20 Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

 A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are
25 characterized by their ability to inhibit the release of

follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of
5 the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the
10 protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United
15 States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

 Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-
25 782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et

al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have
5 chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to
10 mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes,
15 monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly
20 or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing
25 such protein or peptide in any known assay for cell

chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will
5 identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for
10 movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta
15 Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

20 Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such
25 as hemophilias) or to enhance coagulation and other

hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions
5 resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity
10 include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without
20 limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their
25 ligands) and receptor/ligand pairs involved in antigen

presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity

may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly

(such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

10 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without
15 limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);
20 effecting biorhythms or cardiac cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other

nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold

Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

Human liver cDNA library (WO 98/21328) and human stomach cancer cDNA library (WO 98/21328), as well as the cDNA libraries constructed from human kidney mRNA (Clontech), human thymus mRNA (Clontech) and human umbilical cord blood mRNA were used as cDNA libraries.

Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic domain. A clone that has a hydrophobic region

being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

5 The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_mT rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was
10 carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T_mT rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached
15 to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [³⁵S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried out by adding 2.5 µl of a canine pancreas microsome fraction
20 (Promega) to the reaction system. To 3 µl of the reaction solution was added 2 µl of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes
25 and then subjected to SDS-polyacrylamide gel electrophoresis.

The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression in COS7

Escherichia coli cells harboring the expression
5 vector for the protein of the present invention were
cultured at 37°C for 2 hours in 2 ml of the 2 x YT culture
medium containing 100 µg/ml of ampicillin, the helper phage
M13K07 (50 µl) was added thereto, and the cells were then
cultured at 37°C overnight. Single-stranded phage particles
10 were obtained by polyethylene glycol precipitation from a
supernatant separated by centrifugation. The particles were
suspended in 100 µl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from monkey kidney,
COS7, were cultured at 37°C in the presence of 5% CO₂ in the
15 Dulbecco's modified Eagle's medium (DMEM) containing 10%
fetal calf serum. 1 x 10⁵ COS7 cells were inoculated into a
6-well plate (Nunc, well diameter: 3 cm) and cultured at
37°C for 22 hours in the presence of 5% CO₂. After the medium
was removed, the cell surface was washed with a phosphate
20 buffer solution followed by DMEM containing 50 mM Tris-
hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 µl
of the single-stranded phage suspension, 0.6 ml of the DMEM
medium and 3 µl of TRANSFECTAM™ (IBF) was added to the cells
and the cells were cultured at 37°C for 3 hours in the
25 presence of 5% CO₂. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO₂. After the medium was exchanged for a medium containing
5 [35S]cysteine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4) Preparation of Antibodies

10 A plasmid vector containing the cDNA of the present invention was dissolved in a phosphate buffer solution (PBS: 145 mM NaCl, 2.68 mM KCl, 8.09 mM Na₂HPO₄, 2 mM KH₂PO₄, pH 7.2) to a concentration of 2 µg/µl. 25 µl each (a total of 50 µl) of the thus-prepared plasmid solution in
15 PBS was injected into the right and left musculi quadriceps femoris of three mice (ICR line) using a 26 guage needle. After similar injections were repeated for one month at intervals of one week, blood was collected. The collected blood was stored at 4°C overnight to coagulate the blood,
20 and then centrifuged at 8,000 x g for five minutes to obtain a supernatant. NaN₃ was added to the supernatant to a concentration of 0.01% and the mixture was then stored at 4°C. The generation of an antibody was confirmed by immunostaining of COS7 cells into which the corresponding
25 vector had been introduced or by Western blotting using a

cell lysate or a secreted product.

(5) Clone Examples

<HP03171> (SEQ ID NOS: 1, 11 and 21)

Determination of the whole base sequence of the
5 cDNA insert of clone HP03171 obtained from cDNA library of
human thymus revealed the structure consisting of a 90-bp
5'-untranslated region, a 804-bp ORF, and a 1148-bp 3'-
untranslated region. The ORF encodes a protein consisting of
267 amino acid residues and there existed one putative
10 transmembrane domain. Figure 1 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 34 kDa that was somewhat larger than the molecular weight
15 of 30,234 predicted from the ORF. In this case, the
addition of a microsome led to the formation of a product of
38 kDa. In addition, there exists in the amino acid sequence
of this protein one site at which N-glycosylation may occur
(Asn-Thr-Thr at position 169).

20 The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to chicken putative transmembrane
protein E3-16 (Accession No. AAB70816). Table 3 shows the
comparison between amino acid sequences of the human protein
25 of the present invention (HP) and chicken putative

transmembrane protein E3-16 (GG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.0% in the entire region.

Table 3

10 HP MVKISFQPAVAGIKGDKADKASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY
 ***.**.*.* . *.*..... . *. *.*.. .. *.
 GG MVKVSFNSALAH--KEAANKEEENSQVL-ILPPDAKEPEDVVVPAGHKRAWCWCM--CF

HP LSMGMVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSL----SSQVRTQM--

15 *..*.*.....*.*.**..* . .* **.* **.* ..*.....
 GG --GLAFMLAGVILGGAYLYKYFAFQQ--GGVYF-CGIKYIEDGLSLPESGAQLKSARYH

HP ELEEDVKIYLDENYERINVPVPQFGGDPADI IHDFQRGLTAYHDISLDKCYVIELNTTI
 ..*.....* .*. *.*.****.*...****.* **.* **.* **.* **.* **.* **.* **.* **.*

20 GG TIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRRLTAYLDLSLDKCYVIPLNTSV

HP VLPPRNFWELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLRR
 *.**.* **.*.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*

GG VMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENV DQLGFFIYRLCRGKETYKLQR

HP RATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

..... *.**.* **. ***** *.*****

GG KEAMKGIQKREAVNCRKIRHFENRFAMETLICEQ

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL036384) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03424> (SEQ ID NOS: 2, 12 and 22)

Determination of the whole base sequence of the cDNA insert of clone HP03424 obtained from cDNA library of human liver revealed the structure consisting of a 4-bp 5'-untranslated region, a 1260-bp ORF, and a 169-bp 3'-untranslated region. The ORF encodes a protein consisting of 419 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight

of 46,375 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein six sites at which N-glycosylation may occur
5 (Asn-Ala-Ser at position 29, Asn-Val-Thr at position 40, Asn-Cys-Thr at position 112, Asn-Lys-Ser at position 135, Asn-Ile-Ser at position 172 and Asn-Phe-Ser at position 189). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to
10 expect that the mature protein starts from aspartic acid at position 28.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH
15 protein (Accession No. Q06003). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Drosophila melanogaster* GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that
20 of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 40.8% in the intermediate region of 218 amino acid residues.

Table 4

	HP	MSCAGRAGPARLAALALLTCSLWPARADNASQEYOTALINVTVQEPGRGAPLTFRIDRGR
5	HP	YGLDSPKAEVRGQVLAPLPLHGVADHLGCDPQTRFFVPPNIKQWIALLRGNCTFKEKIS
	HP	RAAFHNAVAVVIYNNKSKEEPVTMTHPGTGDI IAVMITELRGKDILSYLEKNISVQMTIA
		. * ** . . * . * . * . * . * . *
	DM	MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGYNVTISII
10		
	HP	VGTR--MPPKNFSRGS LVFSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRR LGDAA
		* * * . * . * * * * * * * . * * * * * . * . * . * . * . *
	DM	EGRRGVRTISSLNRTSVLFVSISFIVDDIL--CWLIFYIQRFRYMQAKDQQSRNLCSVT
15	HP	KKAISKLTTRTVKKGDKETDPDFDHCAVCIESYKQNDVVRI LPCKHVFHKSCVDPWLSEH
		**** * . * . * * . * * . * * * * * * * * . * . * * * * * * * * * * * *
	DM	KKAIMKIPTKTGKFS--EKDLDSDCCAICIEAYKPTDTIRILPCKHEFHKNCIDPWLIEH
	HP	CTCPMCKLNILKALGIVPNLPCTDNVAFDMERLTRTQAVNRRSALGDLAGDNSLGLEPLR
20		***** . ** * * . * . ** .
	DM	RTCPMCKLDVLKFGYVVGDIYQTPS--PQHTAPIASIEEVPVIVVAVPHGPQLQLPLQ
	HP	TSGISPLPDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLNANEVEW
		. * . * . .
25	DM	ASNSSFAPSHYFQSSRSPSSSVQQQLAPLTYQHPQQAASERGRNSAPATMPHAITAS

HP F

DM HQVTDV

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA082118) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03444> (SEQ ID NOS: 3, 13 and 23)

15 Determination of the whole base sequence of the cDNA insert of clone HP03444 obtained from cDNA library of human kidney revealed the structure consisting of a 209-bp 5'-untranslated region, a 1248-bp ORF, and a 460-bp 3'-untranslated region. The ORF encodes a protein consisting of 20 415 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product 25 of 43 kDa that was somewhat smaller than the molecular

weight of 45,691 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 42 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 24.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human type I procollagen C-proteinase enhancer protein (Accession No. BAA23281). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human type I procollagen C-proteinase enhancer protein (CP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.6% in the entire region.

Table 5

HP	M R G A N A W A P L C L L L A A A T Q L S R Q Q S P E R P V F T C G G I L T G E S G F I G S E G F P G V Y P
	* **. * * **** *** ..****...*****..**
CP	M L P A A T A S L L G P L L T A C A L L P F A - Q - G Q T P N Y T R P V F L C G G D V K G E S G Y V A S E G F P N L Y P

HP PNSKCTWKITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNGH-ANGQRIGRFCGTFRPG

. *.*.**. * *.*.***. ****. *. * ..***.*****.

CP PNKECIWTITVPEGQTVSLSFRVFDLELHPACRYDALEVFAGSGTSGQRLGRFCGTFRPA

5 HP ALVSSGNKMMVQMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDR

. **.. **.. ..*..*..*.*.**. .*.*.*** *..* ..*..*****..

CP PLVAPGNQVTLRMTTDEGTGGRGFLWYSGRATSGTEHQFCGGRLEKAQGTLTTPNWPES

HP DYPAGVTCVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGD

10 ***.*.* ***.** .*.*.*****.*.****** *.*****. *.**.*.*.***

CP DYPPGISCSWHIIAPPDQVIALTFEKFDLEPD TYCRYDSVSVFNGAVSDDSRRLGKFCGD

HP SPPAPIVSEARNELLIQFLSDLSTADGFIGHYIFRPKKLPITTE-----

. * . * ** ***** ** . ***** . ***** . * *

15 CP AVPGSISSEGNELLVQFVSDLSVTADGFSASYKTLPRGTAKGQGPGRGTEPKVKLPP

HP QPVTTFPVTGLKTTVALCQQKCRRTGTLEGNYCSSDFVLAGTVITTITRDG-SLHATV

..... *.....*.*.*.*.....*.*.*

CP KSQPPEKTEESPSAPDAPTCPKQCRRTGTLQSNFCASSLVVTATVKSMVREPGEGLA VTV

20 .
HP SIINIYKEGNLAIQAGKNMSARLTVVCKQCPLLRGLNYIIMGVGEDGRGKIM-PNSF

*. *. ** * * . . . * . * ***** . . * . * . *** * * . ** . * . **

CP SLIGAYKTGGLDLPSPPTGASLKFYVPCQCPPMKKGVSYLLMGQV-EENRGPVLPPESE

25 HP IMMFKTKNQKLLDALKNKQC

... ..*..*....*

CP VVLRPNQDQILTNL SKRKCPSPVRAAASQD

5 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. D78874) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
10 encode the same protein as the protein of the present
invention.

<HP03478> (SEQ ID NOS: 4, 14 and 24)

Determination of the whole base sequence of the
cDNA insert of clone HP03478 obtained from cDNA library of
15 human umbilical cord blood revealed the structure consisting
of a 224-bp 5'-untranslated region, a 1143-bp ORF, and a
891-bp 3'-untranslated region. The ORF encodes a protein
consisting of 380 amino acid residues and there existed five
putative transmembrane domains. Figure 4 depicts the
20 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of high molecular weight.

 The search of the protein database using the amino
25 acid sequence of the present protein revealed that the

protein was similar to *Halocynthia roretzi* HrPET-1 protein (Accession No. BAA81907). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Halocynthia roretzi* HrPET-1 protein (HR). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.8% in the entire region.

Table 6

HP	MLQTLYDYFWWERLWLPVNLTWADLEDGRVYAKASDLYITLPLALLFLIVRYFFEL
15	. * . ** . ** * . . ** * ** . * . ** . * . *
HR	MDLLMDLYHWFNEKFWLPQNLTWEDLKRTEEKQFGETRDLWLTPLCITVLCIRFSVEK
HP	YVATPLAALLNIKEKTRLRAPPNATLEHFYLTSGKQPKQVEVELLSRQSGLSGRQVERWF
	. * ** . ** . * * . ** . * * ** * . * . * **
20	HR GIARPLGKWLNLSERLHTPPRENIVLEKVYKTITRKPYSQVEDLCKQTGWRKHEINVWF
HP	RRRRNQDRPSLLKKFREASWRFTFYLIAFIAGMAVIVDKPWFYDMKKVWEGYPIQSTIPS
	* . . . ** . * . ** . * . . . ** . * . * . * . . . * . . . ** . . .
HR	RKKNLVGRPTTLTKFQETFWRFAYLTSFFYGLYVMYDQECVWQTEKCFSNYPEDHVLQS

HP Q-YWYYMIELSFYWSLLFSIASDVKRKDFKEQIIHHVATIILISFSWFANYIRAGTLIMA

. *.**.***.*. ***** * .***..****.. *. **.. *..*..

HR KIYYYYLIELAFYSATTLTQFFDVKRKDFWEMFIHHIVTIILLCGSYTLNYSKMGAFILV

5 HP LHDSSDYLLSAKMFNYAGWKNTCNNIFIVFAIVFIITRLVILPFWILHCTLVYPLELYP

.***.*. . * *** .**.. . . * ** *.* *...*****.**.... * . *

HR VHDSADFYIEFAKMGKYANNSLVNMGFISFTISFFLSRLVILPLWIVPSIWFYGIYTYN

HP AFFGYFFNSMMGVLQLLHIFWAYLILRMAHKFITGKLVEDERSDREETESSEGEAAAAG

10******.* *.. *. * ..* . . .*.*.*.*. * .

HR CAMA-WLFCALL-ILQLLHFYWFHIVKAAYASILVGVIERDTRSESEDSSAEDETAKYS

HP GGAKSRLANGHPILNNNHRKND

.*.

15 HR VGSGDYTESNGIHKRVVTAR

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T27334) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25 <HP03499> (SEQ ID NOS: 5, 15 and 25)

Determination of the whole base sequence of the cDNA insert of clone HP03499 obtained from cDNA library of human kidney revealed the structure consisting of a 129-bp 5'-untranslated region, a 1758-bp ORF, and a 86-bp 3'-untranslated region. The ORF encodes a protein consisting of 585 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 63 kDa that was almost identical with the molecular weight of 63,987 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 82 kDa. In addition, there exist in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-Ile-Thr at position 89, Asn-Glu-Thr at position 106, Asn-Ala-Thr at position 189, Asn-Arg-Thr at position 220 and Asn-Ala-Thr at position 315).

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Chinese hamster hypothetical protein 2BE2121 (Accession No. A30227). Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Chinese hamster hypothetical protein 2BE2121 (CH). Therein, the marks of -,

*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a
5 homology of 44.8% in the entire region.

Table 7

```

HP MVCREQLSKNQVWVFAGITCVSVVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG
10                                     ..***.*.
CH                                     SWSENILDYFLRNS

HP QISRRDALEVTWYHAANSKKAMTAALNSNITVLEADVNV EGLGTANETGVPIMAHPTIY
    **.*.*..***** *..* .**.*. ..****. . . . . * * *****..
15 CH QITTEDGAEIIWYHAANHKSQMQEALRSAAHMIEADVLLPS--DGSEHGQPIMAHPPEMN

HP SDNTLEQWLDVAVLGSSQKGIKLD FKNIKAVGPSLDLLRQLTEEGKVRRPIWINADILKGP
    *****..**.*. .*.******.. *.*.*.*..... ..*.*.***.* **
CH SDNTLQEWLAEVM-KSNKGIKLDFKSLAAARASMLFLDNVKQH--LQCPVWMNADVLPGP
20

HP NMLISTEVNATQFLALVQEKYPKATLSPGWTTTFYMSTSPNRTYTQAMVEKMHELVGGV PQ
    * *.*.*..**.*.*.*.* ***** . . . *.*.*..**.*. . .**.*
CH NG-SSKVVDAKAFLDTVTSFFPDVTFSLGWTTGWHPKVN EGYSWTMVKEMDYICSLTQ
25

HP RVTFPVRSSMVRAAWPHFSWLLSQSERYSLTLWQAASDPMSVEDLLYVRDNTAVHQVYYY

```

```

*****...**... ***...*.*****.*...*. *****.**...**. **
CH PVTFPVRAALVRQSCSQLLWLLKKNRYSLTVWTGKDDSYPTEDLLYIRDYFNKTQVFYD

HP IFEPLLSQFKQLALNATRKPYYTGGSLIPLLQLPGDDGLNVEWLVPDVQSGKTATMTL

5    *.**...***
CH ILEPQSHEFKQAIGI

```

Furthermore, the search of the GenBank using the
 10 base sequences of the present cDNA has revealed the
 registration of sequences that shared a homology of 90% or
 more (for example, Accession No. R92398) among ESTs. However,
 since they are partial sequences, it can not be judged
 whether or not they encode the same protein as the protein
 15 of the present invention.

<HP03500> (SEQ ID NOS: 6, 16 and 26)

Determination of the whole base sequence of the
 cDNA insert of clone HP03500 obtained from cDNA library of
 human kidney revealed the structure consisting of a 134-bp
 20 5'-untranslated region, a 996-bp ORF, and a 476-bp 3'-
 untranslated region. The ORF encodes a protein consisting of
 331 amino acid residues and there existed one putative
 transmembrane domain at the N-terminus. Figure 6 depicts the
 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
 25 Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 37,694 predicted from the ORF.

5 The search of the protein database using the amino acid sequence of the present protein revealed that the amino acid sequence of the protein matched with that of human hypothetical protein (Accession No. AAC05803) in which a region of 62 amino acid residues from glycine at position 88 to lysine at position 149 was deleted.

10 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340631) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
15 encode the same protein as the protein of the present invention.

<HP10691> (SEQ ID NOS: 7, 17 and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10691 obtained from cDNA library of
20 human umbilical cord blood revealed the structure consisting of a 246-bp 5'-untranslated region, a 1038-bp ORF, and a 1096-bp 3'-untranslated region. The ORF encodes a protein consisting of 345 amino acid residues and there existed at least two putative transmembrane domains. Figure 7 depicts
25 the hydrophobicity/hydrophilicity profile, obtained by the

Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human BB1 protein (Accession No. AAB37433). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human BB1 protein (BB). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The C-terminal region of 215 amino acid residues of the present protein shared a homology of 81.9% with the N-terminal region of human BB1 protein.

Table 8

	HP	MSPEEWTYLVLLISIPIGFLFKKAGPGLKRWGAAAVGLGLTLFTCGPHTLHSLVTILGT.
20	HP	WALIQAQPCSCHALALAWTFSYLLFFRALSLGLPTPTPFTNAVQLLLTLKLVSLASEVQ
	HP	DLHLAQRKEMASGFSKGPTLGLLPDVPSLMETLSYSYCYVGIMTGPFPRYRTYLDWLEQP
		*****. . . * . * . *
25	BB	MASGFSKGPTLGLLRALPDGDT-QLQLLLRGNHDRPVLPPLPGLAGAA

HP FPGAVPSLRPLLRRRAWPAPLFGLLFLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

. * . . *****

BB LPRGSASLRPLLRRRAWPAPLFGLLFLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

5

HP FRMRFYVAWIAAECGCIAAGFGAYPVAAKARAGGGPTLQCPPSSPEKAASLEYDYETIR

BB FRMRFYVAWIAAECGCIAAGFGAYPVAAKARAGGGPTLQCPPSSPEKAASLEYDYETIR

10

HP NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRL

BB NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRTAWTMLSAYWHGLHP

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W48653) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

20

encode the same protein as the protein of the present invention.

<HP10703> (SEQ ID NOS: 8, 18 and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10703 obtained from cDNA library of

25

human kidney revealed the structure consisting of a 359-bp

5'-untranslated region, a 270-bp ORF, and a 1388-bp 3'-untranslated region. The ORF encodes a protein consisting of 89 amino acid residues and there existed one putative transmembrane domain. Figure 8 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18 kDa that was larger than the molecular weight of 10,469 predicted from the ORF.

10 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T08343) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
15 encode the same protein as the protein of the present invention.

 <HP10711> (SEQ ID NOS: 9, 19 and 29)

 Determination of the whole base sequence of the cDNA insert of clone HP10711 obtained from cDNA library of
20 human kidney revealed the structure consisting of a 29-bp 5'-untranslated region, a 1221-bp ORF, and a 356-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative
25 transmembrane domain at the N-terminus. Figure 9 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 44 kDa that was almost identical with the molecular weight of 43,836 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein seven sites at which N-glycosylation may occur (Asn-Ser-Thr at position 65, Asn-Trp-Ser at position 95, Asn-Val-Ser at position 134, Asn-Ile-Thr at position 159, Asn-Gly-Ser at position 187, Asn-Arg-Ser at position 230 and Asn-Leu-Thr at position 333). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 36.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse kidney predominant protein (Accession No. BAA92527). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse kidney predominant protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The

both proteins shared a homology of 79.9% in the entire region.

Table 9

5

HS MRGSVECTWGWGHCAPSPLLLWTL LLFAAPFGLLGEKTRQVSLEVIPNWLGP LQNLLHIR

* *** . *** . * ** . ** . ***** ** . ***** . *** . . * . * *****

MM MFRCWGP HWGWPCAPTPWLLSLLVCSAPFGLQGEETRQVSMEVISGWPNP-QNLLHIR

10

HS AVGTNSTLHYVWSSLG PLAVVMVATNTPHSTLSVNWSLLLSPEPDGGLMVL PKDSIQFSS

*** . ***** ***** . * . ***** . * . * . ***** . *****

MM AVGSNSTLHYVWSSLGPPAVVLVATNTTQSVLSVNWSLLLS PDPAGALMVL PKSSIQFSS

HS ALVFTRLLEFDSTNVSDTA AKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMND

15

***** . * . . * . * . ***** . ***** . *** * . *** . *** . * . *

MM ALVFTRLLEFDSTNASE-GAQPPGKPYPPYSLAKFSWNNITNSLDLANLSADFQGRPVDD

HS PTRTFANGSLAFRVQAFSRSSRPAQP PRLHTADTCQLEVALIGASPRGNRSLFGLEVAT

** . ***** . * . ***** . ***** . ***** . ***** . *****

20

MM PTGAFANGSLTFKVQAFSRSGRPAQP PRLHTADV CQLEVALVGASPRGNHSLFGLEVAT

HS LGQGPDCPSMQEQHSIDDEYAPAVFQLDQLLWGS LPSGFAQWRPVAYSQKPGGRESALPC

***** . * . ***** . ***** ***** ***** . * . . *****

MM LGQGPDCPSVNERNSIDDEYAPAVFQLNQLLWGSSPSGFMQWRPVAFSEERAREALPC

25

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse calcium channel gamma 5 subunit (Accession No. CAB86387). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse calcium channel gamma 5 subunit (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 75.0% in the entire region.

Table 10

	HS	MTAVGVQQRPLGQRQPRRSFFESFIRTLIITCVALAVVLSSVSICDGHWLLAEDRLFGL
20		***.*.**. ** ..*.*****.*.*****.**,****
	MM	MTAIGAQAHKLLGLKRPHRSFFESFIRTLIIVCTALAVVLSSVSICDGHWLLVEDHLFGL
	HS	WHFCTTTNQSVPICFRDLGQAHPGLAVGMGLVRSVGALAVVAAIFGLEFLMVSQLEDK
		*.***.*.*.*.***.***.*****.***.*.*****.*.***.***
25	MM	WYFCTIGNHSEPHCLRDLSQAHPGLAVGMGLARSAAMAVVAAIFGLEMLIVSQCEDV

HS HSQCKWVMGSILLVSVFLSSGGLLGFVILLRNQVTLIGFTLMFWCEFTASFLFLNAIS

. *. **. ** ****. *. ****. *. *. *. *. ****. **** *

MM RSRRKWAIGSYLLLVAFILSSGGLLTFIILLKNQINLLGFTLMFWCEFTASFLFLNAAS

5

HS GLHINSITHPWE

****. *. **.

MM GLHINSLTQPWDPAGTLAYRKRGYDGTSLI

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA910339) among ESTs.

15 However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03010> (SEQ ID NOS: 31, 41 and 51)

Determination of the whole base sequence of the
 20 cDNA insert of clone HP03010 obtained from cDNA library of human kidney revealed the structure consisting of a 97-bp 5'-untranslated region, a 1134-bp ORF, and a 320-bp 3'-untranslated region. The ORF encodes a protein consisting of 377 amino acid residues and there existed at least eight
 25 putative transmembrane domains. Figure 11 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was almost identical with the molecular weight of 41,462 predicted from the ORF as well as a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Arabidopsis thaliana* hypothetical protein (Accession No. AAC34490). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Arabidopsis thaliana* hypothetical protein (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 42.0% in the entire region other than the N-terminal region.

Table 11

HP MDSALSDPHNGSAEAGGPTNSTTRPPSTPEGIALAYGSLLLALLPIFFGALRSVRCARG

* * *

25 AT MKNCERFANLALAGLTLAPLVVRVNPNLNVILTACITYVYGCFRS

HP KNASDMPETITSRDAARFPIIASCTLLGLYLFFKIFSQEYINLLSMYFFVLGILALSHT

```

...  .**...  . * ***... *  **,*,*,*,**...*,...  . * .*,  *****,** *

```

AT VKDTPPTETMSKEHAMRFPLVGSAMLLSLFLFKFLSKDLVNAVLTAYFFVLGIVALSAT

5

HP ISPFMNKFFPASFPNRQYQLLFTQGSGENKEEIINYEFDTKDLVCLGLSSIVGVWYLLRK

. * . . . * * * . . . * * . . . * . . . * * . *

AT LLPAIRRF LNPWN DLIVWRF-----PYFKSLEVEFTKSQVVAGIPGTFFCAWYAWKK

10 HP HWIANNLFLAFLSLNGVELLHLNNVSTGCILLGGLFIYDVFVWFGTNVMVTVAKSFEAPI

,, . **, *. . . *, *. * *, . . ** ***, ***, **, ***** * ***, *****, *****

AT HWLANNILGLSFCIQGIEMLSLGSFKTGAILLAGLFFYDIFWVFFTPVMVSVAKSFDAP

HP KLVFPQDLLEKGLEANNFAMGLGDVVIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF

```
15      **, ** .      ..* .      ..*****.*****. ** *****.* ..... ** ..* .*
```

AT KLLFPTG---DALRP--YSMLGLGDIVIPGIFVALALRFDVSRRRQPQ-YFTSAFIGYAV

HP GLGLTIFIMHIFKHAQPALLYLPACIGFPVLVALAKGEVTEMFSYEESNPKDPAAVTES

*. *** .*. *. *****.*** ***, . . *. ** . . . *. **

20 AT GVILTIVVMNWFQAAQPALLYIVPAVIGFLASHCIWNGDIKPLLAFDESKTEE-ATTDES

HP KEGTEASASKGLEKKEK

* . . . *

AT KTSEEVNKAHDE

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA380429) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03576> (SEQ ID NOS: 32, 42 and 52)

Determination of the whole base sequence of the cDNA insert of clone HP03576 obtained from cDNA library of human kidney revealed the structure consisting of a 88-bp 5'-untranslated region, a 246-bp ORF, and a 1379-bp 3'-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed two putative transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 9,178 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human vacuolar proton ATPase 9 kDa (Accession No. NP_003936). Table 12 shows the comparison

between amino acid sequences of the human protein of the present invention (HP) and human vacuolar proton ATPase 9 kDa (VP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 71.2% in the entire region.

10 Table 12

HP MTAHSFALPVIIFTTFWGLVGIAGPWFVPKGNRGVIITMLVATAVCCYLFWLIAILAQL

*. *. *. ***. **. ***. *****. *****

VP MAYHGLTVPLIVMSVFWGFVGLVPWFIPKGNRGVIITMLVTCSVCCYLFWLIAILAQL

15

HP NPLFGPQLKNETIWYVRFWE

*****... *

VP NPLFGPQLKNETIWYLYHWP

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W22566) among ESTs. However, since they are partial sequences, it can not be judged

whether or not they encode the same protein as the protein of the present invention.

<HP03611> (SEQ ID NOS: 33, 43 and 53)

Determination of the whole base sequence of the
5 cDNA insert of clone HP03611 obtained from cDNA library of human kidney revealed the structure consisting of a 189-bp 5'-untranslated region, a 1464-bp ORF, and a 105-bp 3'-untranslated region. The ORF encodes a protein consisting of
10 transmembrane domains. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

15 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human cystine/glutamate transporter (Accession No. BAA82628). Table 13 shows the comparison between amino acid sequences of the human protein of the
20 present invention (HP) and human cystine/glutamate transporter (CG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present
25 invention, respectively. The both proteins shared a homology

of 43.8% in the entire region other than the N-terminal region.

Table 13

5

HP MGD TGLRKRREDEKSIQSQEPKTTSLQELGLISGISIIVGTIIGS

.....*.....*.*.***.*****.

CG MVRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLKRKVTLLRGVSIIGTIIGA

10 HP GIFVSPKSVLSNTEAVGPCLIIWAACGVLATLGALCFAELGTMITKSGGEYPYLMEAYGP

***** ** . ** . * . * . * . * . * . * . * . * . * . *

CG GIFISPKGVLQNTGSVGMSLTIWTVCGVLSLFGALS Y AELGTTIKKSGGHYTYILEVFGP

HP IPAYLFSWASLIVIKPTSFAIICLSFSEYVCAPFYVGCKPPQIVVKCLAAAAILFISTVN

15 .**.. *.**..**.. *.**..* *.**..* *.**..* ..**..* ..**..* ..**..*

CG LPAFVRVWVELLIIRPAATAVISLAFGRYILEPFFIQCEIPELAIKLITAVGITVVMVLN

HP SLSVRLGSYVQNIFTAAKLIVIVAIIIIISGLVLLAQGN TKNFDNSFEQAQLSVGAISLAFY

*_**_ . _ . * _ . * **_ . ***_ . *_ . * _ . *_ . *_ . *_ . *_ . *_ . *_ . *

20 CG SMSVSW SARIQIFLTFCKLTAILIIIVPGVMQLIKGTQNFKDAFSGRDSSITRLPLAFY

HP NGLWAYDGNQLNYITEELRNPNRNLPLAIIIGIPLVTACYILMNVSYFTVMTATELLQS

*..**.* **..**.* ** ..*** **...** **.* **.***.*..*.***.* *

CG YGMYAYAGWFYLNFTVEENPEKTIPLAICISMAIVTIGYVLTNAVYFTTINAEELLS

25

HP QAVAVTFGDRVLYPASWIVPLFVAFSTIGAANGTCFTAGRLIYVAGREGHMLKVLSYISV

.*****.*.* * *.**.*.*.*. *.**.*...**.***.***.*. ..**.* *

CG NAVAVTFSERLLGNFSLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV

5 HP RRLTPAPAIIFYGIIATIIYIIPGDINSLVNYFSFAAWLFYGLTILGLIVMRFRKELERP

*. **.*.* .. * ...**.***.*...*** **.*. ***.*.. ...**

CG RKHTPLPAVIVLHPLTMIMLFSGDLDLNLNLSFARWLFGLAVAGLIYLRYPKCPDMHRP

HP IKVPVVIPVLMTLISVFLVLAPIISKPTWEYLYCVLFILSGLLFYFLFVHY—KFGWAQK

10 .***. **.*.....*.* .. *.**.*. *.*.*. . * * .

CG FKVPLFIPALFSFTCLFMVALSLYSDP—FSTGIGFVITLTGVPAYYLFIIWDKKPRWFRI

HP ISKPITMHLQMLMEVVPPEEDPE

.*. **. **...**** *

15 CG MSEKITRTLQIILEVVPEEDKL

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R07056) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25 <HP03612> (SEQ ID NOS: 34, 44 and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03612 obtained from cDNA library of human kidney revealed the structure consisting of a 153-bp 5'-untranslated region, a 1128-bp ORF, and a 269-bp 3'-untranslated region. The ORF encodes a protein consisting of 375 amino acid residues and there existed seven putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 39 kDa that was somewhat larger than the molecular weight of 37,930 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human monocarboxylate transporter (Accession No. AAC70919). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human monocarboxylate transporter (MC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the N-terminal region of 192 amino acid residues.

Table 14

	HP	MTPQPAGPPDGGWGWVAAAAFAINGLSYGLLRSLGLAFPDLAEHFDRSAQDTAW
		. * . * * * * * . * . * . * * . * . * * . . . * . . . * .
5	MC	MPPMPSAPPVHPPPDGGWGWIVVGATFISIGFSYAFPKAVTVFFKEIQQIFHTTYSEIAW
	HP	ISALALAVQQAASPVGSALSTRWGARPVVMVGGVLASLGFVFSAFASGLLHLYLGLGLLA
		* * . * * * * . * * . * . * . . . * . * * * . * . * . . . * . * . . . * . * . . .
	MC	ISSIMLAVMYAGGPVSSVLVNKYGSRPVVIAGLLCCLGMVLASFSSSVVQLYLTMGFIT
10	HP	GFGWALVFAPALGTLSTRYFSRRRVLAVGLALTGNGASSLLLAPALQLLLDTFGWRGALLL
		* . * . * . . . * * * * . * . * . * . * . * . * . * . * . * . * . * . * .
	MC	GLGLAFNLQPALTIIGKYFYRKRPMANGLAMAGNPVFLSSLAPFNQYLFNTFGWKGSFLI
15	HP	LGAITLHLTPCGALLLPLVLPGDPPAPPRSPLAALGLSLFTRRAFSIFALGTALVGGGYF
		* * . . * . * . * . * *
	MC	LGSLLLNACVAGSLMRPLGPNQTTSKSKNKTGKTEDDSSPKIKTKKSTWEKYNKYLDFS
	HP	VPYVHLAPRFRPGPGGIRSSAGGGRGCDGGCGRPAGLRVAGRPRLGAPPAAAGRIRGSDW
20	MC	LFKHRGFLIYLSGNVIMFLGFFAPIIFPAPYAKDQGIDEYSAAFLLSVMAFVDMFARPSV
	HP	AGAVGGGAGARGRRRELGGSPAGRGCLWAERGELRPAGFRCTPRAGGRRRCGAGHRAG
25	MC	GLIANSKYIRPRIQYFFSFAIMFNGVCHLLCPLAQDYTSVLVYAVFFGLGFGSVSSVLFE

HP DDADEPRGAPGPSVRLPKG

MC TLMDLVGAPRFSSAVGLVTIVECGPVLLGPPLAGKLVDLTGEYKMYMSCGAIVVAASVW

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI742291) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10407> (SEQ ID NOS: 35, 45 and 55)

15 Determination of the whole base sequence of the cDNA insert of clone HP10407 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 100-bp 5'-untranslated region, a 1053-bp ORF, and a 332-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed at least four putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

25 The search of the protein database using the amino acid sequence of the present protein revealed that the

protein was longer by 35 amino acid residues at the N-terminus than human hypothetical protein (Accession No. CAB43375).

Furthermore, the search of the GenBank using the
5 base sequences of the present cDNA has revealed the registration of a clone beginning from the 117th base of the present cDNA (Accession No. AL050274).

<HP10713> (SEQ ID NOS: 36, 46 and 56)

Determination of the whole base sequence of the
10 cDNA insert of clone HP10713 obtained from cDNA library of human kidney revealed the structure consisting of a 79-bp 5'-untranslated region, a 2004-bp ORF, and a 611-bp 3'-untranslated region. The ORF encodes a protein consisting of 667 amino acid residues and there existed nine putative
15 transmembrane domains. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

20 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse retinoic acid-responsive protein (Accession No. AAC16016). Table 15 shows the comparison between amino acid sequences of the human protein
25 of the present invention (HP) and mouse retinoic acid-

responsive protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.1% in the entire region.

Table 15

10 HP MSSQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLAS
 *.***.*.*.*** ****.*.*.***.*.*.***.*.*.***.*
 MM MESQASENGSQTSSGVTDDYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLAS

HP LSILVLLLLAMLVRRRQLWPDCVRGRGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLL
 15 **.*****,*****.*** * . ***** ..*****.**.*.***
 MM LSFLVLLLLALLVRRRRLWPRCGHRGLGLSPVDFLAGDLSWTVPAAVFVLFNSLCLLL

HP PDEDALPFLTASAPSQDGKTEAPRGAWKILGLFYAALYYPLAACATAGHTAAHLLGST
 ,**,*.*.*.*.*. *.*.***.*.*.*.*.*****.*** ** ***,.
 20 MM PDENPLPFLNLTAASSPDGEMETSRGPWKLLALLYYPALYYPLAACASAGHQAFLGTV

HP LSWAHLGVQVWQRAECPQVPKIYKYSSLLASLPLLGLGFLSLWYPVQLVRSFSRRTGAG
 *****,*****,***** *****,*****.***.*.***
 MM LSWAHFGVQVWQKAECQDPKIYKHYSLLASLPLLGLGFLSLWYPVQLVQSLRHRTGAG

HP SKGLQSSYSEEYLRNLLCRKKLGSSYH-TSKHGFLSWARVCLRHCIYTPQPGFHLPLKLV

*, ***, ****, ****, ****, ***, *, * . **... ***, *.. . *, *****, *****,

MM SQGLQTSYSEKYLRTLLCPKKLDSCSHPAKRSLLSRAWAFSHHSIYTPQPGFRLPLKLV

5 HP LSATLTGTAIYQVALLLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKH

, *****, *****, *****, *****, . *****, *****,

MM ISATLTGTATYQVALLLLVSVVPTVQKVRAGINTDVSYLLAGFGIVLSEDRQEVVELVKH

HP HLWALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAI

10 ***, . *, *****, *****, *, ***, ***, **, *****, *, * *****,

MM HLWTVEACYISALVLSCASTFLLLIRSLRTHRANLQALHRGAALDLDPPPLQSIHPSRQAI

HP FCWMSFSAYQTAFICLGLLVQIIFFLGTTALAFLVLMFVLHGRNLLFRSLESSWPFWL

, ****, *****, *****, *****, *****, . *, *****, *****, *****,

15 MM VSWMSFCAYQTAFSCLGLLVQVIFFLGTTSLAFLVFVPLLHGRNLLLRSLSTWPFWL

HP TLALAVILQNMAAHWVFLETHDGHPLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSA

*, *****, **, *, ** **, *, *, *****, *, . *****, *, *****, . *, *****, *

MM TVALAVILQNIAANWIFLRTHHGYPELTNRRMLCVATFLLFPINMLVGAIMAVWRVLISS

20

HP LYNAIHLGQMDLSLLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAQSLPR

, . **, *****, *****, **, *****, **, *****, . . *****, *****, *, * **

MM LYNTVHLGQMDLSLLPQRAASLDPGYHTYQNFLEKIEVSQSHPGVIAFCALLHAPSPQPR

25 HP TMAAPQDSLPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKT

. *****. **. ***** ***** . . *. *****. **. **.
 MM PPLAPQDSLPAEEEEGMQLLQTKDLMAKGAGHKGSQSRARWGLAYTLLHNPSLQAFRKA

 HP ALLGANGAQP

 5 **. *.
 MM ALTSAKANGTQP

The search of the GenBank using the base sequences
 10 of the present cDNA has revealed the registration of
 sequences that shared a homology of 90% or more (for example,
 Accession No. AI760170) among ESTs. However, since they are
 partial sequences, it can not be judged whether or not they
 encode the same protein as the protein of the present
 15 invention.

<HP10714> (SEQ ID NOS: 37, 47 and 57)

Determination of the whole base sequence of the
 cDNA insert of clone HP10714 obtained from cDNA library of
 human umbilical cord blood revealed the structure consisting
 20 of a 82-bp 5'-untranslated region, a 1395-bp ORF, and a
 1820-bp 3'-untranslated region. The ORF encodes a protein
 consisting of 464 amino acid residues and there existed a
 putative secretory signal at the N-terminus. Figure 17
 depicts the hydrophobicity/hydrophilicity profile, obtained
 25 by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 49 kDa that was somewhat smaller than the molecular weight of 52,340 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 52 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ala-Thr at position 164 and Asn-Asp-Ser at position 320). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from threonine at position 22.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA861134) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10716> (SEQ ID NOS: 38, 48 and 58)

Determination of the whole base sequence of the cDNA insert of clone HP10716 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 60-bp 5'-untranslated region, a 1413-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein consisting of 470 amino acid residues and there existed one

putative transmembrane domain at the N-terminus. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 61 kDa that was larger than the molecular weight of 52,086 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein CGI-90 (Accession No. AAD34085). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein CGI-90 (CG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the entire region.

Table 16

HP MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG

HP RHVMLLRVPGGAGDASVLPSPREGQEKVLDRLDFVLTSLVALRREVEELRSSLRGLAG

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA852295) among ESTs. However, since they are
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10717> (SEQ ID NOS: 39, 49 and 59)

Determination of the whole base sequence of the
10 cDNA insert of clone HP10717 obtained from cDNA library of human kidney revealed the structure consisting of a 73-bp 5'-untranslated region, a 732-bp ORF, and a 976-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed two putative
15 transmembrane domains. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was larger than the molecular weight of
20 26,270 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI478174) among ESTs. However, since they are
25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10718> (SEQ ID NOS: 40, 50 and 60)

Determination of the whole base sequence of the
5 cDNA insert of clone HP10718 obtained from cDNA library of
human umbilical cord blood revealed the structure consisting
of a 86-bp 5'-untranslated region, a 813-bp ORF, and a 889-
bp 3'-untranslated region. The ORF encodes a protein
consisting of 270 amino acid residues and there existed
10 three putative transmembrane domains. Figure 20 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 28 kDa that was smaller than the molecular weight of
15 31,116 predicted from the ORF.

The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to *Caenorhabditis elegans* hypothetical
protein Y53C10A (Accession No. CAA22139). Table 17 shows the
20 comparison between amino acid sequences of the human protein
of the present invention (HP) and *Caenorhabditis elegans*
hypothetical protein Y53C10A (CE). Therein, the marks of -,
*, and . represent a gap, an amino acid residue identical
with that of the protein of the present invention, and an
25 amino acid residue similar to that of the protein of the

present invention, respectively. The both proteins shared a homology of 54.8% in the entire region other than the N-terminal region.

5 Table 17

	HP	MAGAEDWPGQ
	CE	MTSSSAASSSTTTSTTSTMPDENECLKKEERFKSPDPAPTLDEEVDIDTLPSMLEDDPNG
10	HP	QLELDEDEASCCRWGAQHAGARELAALYSPGKRLQEWCSVILCFSLIAHNLVHLLLLARW
		.**..**..** .***** *.. . *.. ... ***. *
	CE	NVVECDLGFKGPRWGPQHAGAKKLASMYSKEKRLQEKVSLFAAIFLFSIVFIN-LLLS-W
15	HP	EDT--PLVILGVVAGALIADFLSGLVHWGADTWGSVELPIVGKAFIRPFREHHIDPTAIT
		*.. *....* * ..*** *****.***.***** . *..*****.*****
	CE	ESSIWVSVLVSAVLGIMTADFASGLVHWAADTFGSVE-TWFGRSFIRPFREHHVDPTAIT
	HP	RHDFIETNGDNCLVTLLPLLNMAYKFRTHSPEALEQ--LYPWECFVFCLIIFGTFTNQIH
20		***..*.*****.. . *** . *. *. ..*..* ..* ... * *. ..*****
	CE	RHDIVEVNGDNCMLCVGPLLWILYQQMTYQRDAITQWATFWH--YILLGGIYVALTNQIH
	HP	KWSHTYFGLPRWVTLLQDWHVILPRKHHRIHHVSPHETYFCITTGWLNYPLEKIGFWRRL
		***** **..** .*.****.**.***.***. *.*****.*** *****.
25	CE	KWSHTYFGLPTWVVFLLQKAHIILPRSHHKIHHISPHACYYCITTGWLNPLEYIGFWRKM

HP EDLIQGLTGEKPRADDMKWAQKIK

*** .**.**.*** *..

CE EWVTTVTGMQPREDDLKWATKLQ

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA176107) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, the region from position 466 to position 778 of the cDNA of the present invention matched with the region from position 2 to position 314 of human ubiquitin-conjugating enzyme E2 variant 1 (Accession NO. NM_003349) although no match was observed in another region.

<HP03745> (SEQ ID NOS: 61, 71 and 81)

20 Determination of the whole base sequence of the cDNA insert of clone HP03745 obtained from cDNA library of human kidney revealed the structure consisting of a 99-bp 5'-untranslated region, a 1170-bp ORF, and a 107-bp 3'-untranslated region. The ORF encodes a protein consisting of 389 amino acid residues and there existed at least nine

25

putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 7 (Accession No. NP_003974). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 7 (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.0% in the N-terminal region of 397 amino acid residues.

Table 18

20

HP

MDRGEKIQKRVFGYWWGTSFLLINIIG

.*.***. .. *.*... *.**

SC MEAREPGRPTPTYHLPNTSQSQVEEDVSSPPQRSSETMQLKKEISLLNGVSLVGNMIG

25

HP AGIFVSPKGVLAYSCMNVGVSICVWAGCAILAMTSTLCSAEISISFPCSGAQYYFLKRYF

.*****... . *.** ***** **..... *** * .. *

SC SGIFVSPKGVLVHT-ASYGMSLIVWAIGGLFSVVGALCYAELGTTITKSGASYAYILEAF

HP GSTVAFLNLWTSFLGSGVVAG-QALLAEYSIQPFPPSCSVPKLPKKCLALAMLWIVGI

5 *. **..**..**.. *. .*. * *** ****. * *. . ** *

SC GGFIAFIRLWVSLLVVEPTGQAIITFANYIIQPSFPSCDPPYLACRLAAACICLLTF

HP LTSRGVKEVTWLQIASSVLKVSILSFISLTGVVFLIRGKKENVERFQNAFDAELPDISHL

 ... ** *. * . . ** * * . * . * . * . *.**..**..*... *...*

10 SC VNCAYVKWGTRVQDTFTYAKVVALIAIIVMGLVKLCQG—HSEHFQDAFEGSSWDMGNL

HP IQAIFQGYFAYSG—————ELKKPRTTIPKCIFTALPLVTVVYLLVNISYLTVLTPR

 *.. . *.*** *. * . * * . * . * . * . * . * . * . * . * . *

SC SLALYSALFSYSGWDTLNFVTEEIKNPERNLPLAIGISMPIVTLIYILTNVAYYTVLNIS

15 HP EILSSDAVAITWADRAFPSLAWIMPFAISTSLFSNLLISIFKSSRPIYLASQEGQLPLLF

 ..*****.*.***.* ..*..*..* * *..* *** ****.**.*.***.

SC DVLSSDAVAVTFADQTFGMFSWTIPIAVALSCFGGLNASIFASSRLFFVGSREGHLPDLL

20 HP NTLNSHS-SPFTAVLLLVTLGSLAIILTSLIDLINIIFFTGSLWSILLMIGILRRRYQEP

 *. * . * . * . * . . . * * . . . * . . . * . . *

SC SMIHIERFTPIPALFNCTMALIYLIVEDVFQLINIFYFSFYWFFVGLSVVGQLYLRWKEP

HP NLSIPYKVKLDF

25 . . * * . . *

SC KRPRPLKLSVFFPIVFCICSVFLVIVPLFTDTINSLIGIGIALSGVPFYFMGVLPESRR

<HP03747> (SEQ ID NOS: 62, 72 and 82)

5 Determination of the whole base sequence of the
cDNA insert of clone HP03747 obtained from cDNA library of
human umbilical cord blood revealed the structure consisting
of a 21-bp 5'-untranslated region, a 1047-bp ORF, and a
1324-bp 3'-untranslated region. The ORF encodes a protein
10 consisting of 348 amino acid residues and there existed a
putative secretory signal at the N-terminus and one putative
transmembrane domain at the C-terminus. Figure 22 depicts
the hydrophobicity/hydrophilicity profile, obtained by the
Kyte-Doolittle method, of the present protein. In vitro
15 translation resulted in formation of a translation product
of 40 kDa that was almost identical with the molecular
weight of 39,685 predicted from the ORF. Application of the
(-3,-1) rule, a method for predicting the cleavage site of
the secretory signal sequence, allows to expect that the
20 mature protein starts from proline at position 39.

 The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to human endoplasmic reticulum
glycoprotein (Accession No. NP_006807). Table 19 shows the
25 comparison between amino acid sequences of the human protein

of the present invention (HP) and human endoplasmic reticulum glycoprotein (ER). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 54.1% in the entire region.

Table 19

10

HP MAATLGPLGSWQ-QW-RRCLSARD-----GSRMLLLLLLLGSGQGPQQVGAGQTFEYLK

*. * ****. .. *. *.**** **.. *.**

ER MAEGWIWRWGWGRCLGRPGLLGPGPPTPLFLLLL-LGSVTADITDGNS-EHLK

15

HP REHSLSKPYQGVTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQALWNRVPCFLRDWELQ

***** *****..* .**..*..* .**..***** .**..*..** .***.***..

ER REHSLIKPYQGVGSSSMPLWDFQGSTMITSQYVRLTPDERSKEGSIWNHQPCLKDWEMH

20

HP VHFKEHGQKKNLHGDGLAIWYTKDRMQGPVFGNMDKVFGLGVFVDTPNEEKQQERVF

****. ** *****. *.***. **. *****. *. * **..*.*****. *. ****

ER VHFVHGTGKKNLHGDGIALWYTRDLVPGPVFGSKDNFHLAIFLDTPNDET-TERVF

HP PYISAMVNNGSLSYDHERDGRPTLGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKH

****.*****.*** ***.**** ** ..****.*** . .**.* *...*,

25

ER PYISVMVNNGSLSYDHSKDGRTLAGCTADFRNRDHTFLAVRYSRGRLTVMTDLEDKN

HP EWRDCIEVPGVRLPRGYFSGTSSITGDLSDNHDVISLKLFEITVERTPEEEKLHRDVFLP

****..**...***** *****.*. ****O*****,**,***.* **,**.**..... ***

ER EWKNCIDITGVRLPTGYFFGASAGTGDLSNDHDIISMFLQLMVEHTPDEESIDWTKIEP

5

HP SVDNMKLP-----EMTAPL--PPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK

******, **. * *** **.** *****, **.** ******, ***** ******, **...** **.** *****, ***** ******, ***** **...**, *****, ******, **...** *****

ER SVNFLKSPKDNVDDPTGNFRSGPLTGWRVFLLLCALLGIVVCAVVGAVVFQKRQERN-K

10 HP RFY

ER RFY

15 Furthermore, the search of the GenBank using the
base sequences of the present cDNA has revealed the
registration of sequences that shared a homology of 90% or
more (for example, Accession No. AA262924) among ESTs.
However, since they are partial sequences, it can not be
20 judged whether or not they encode the same protein as the
protein of the present invention.

<HP10719> (SEQ ID NOS: 63, 73 and 83)

Determination of the whole base sequence of the
cDNA insert of clone HP10719 obtained from cDNA library of
25 human kidney revealed the structure consisting of a 54-bp

5'-untranslated region, a 786-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 261 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 33 kDa that was larger than the molecular weight of 27,435 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from asparagine at position 19.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse endomucin (Accession No. AAD05208). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse endomucin (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 47.9% in the entire region.

Table 20

	HP	MELLQVTIL-FLLP-SIC-SSNSTGVL-EAANNSLVTTTKPSITTPNTESLQKNVVTPT
		* ***.*. * ***. *. * *.....****. *. *. *. * . * . *.
5	MM	MRLQATVLFLLSNLCHSEDGKDQVQNDSIPTPAETSTTKASVTIPGIVSV-TNPNKPA
	HP	TGTPKGTITNELLKMSLMSTATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPLNAV
		..*. *. *. *..... . *. * . *. .. . *.. . *. * . .. *.. . *..
	MM	DGTPPEGTTKSDVSQTSVLTINSLTTPKHEVGTTTEGPLRNESSTMKITVPNTPTSAN
10	HP	STLQSSPKKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENTSQSQVIGTEGG
		***. *. *. *..* *. ** * . *..
	MM	STLPGSQNKITTQ-----LLDALPKITATPS-----ASLTTAHTMSLLQDTEDR
15	HP	KNASTSATSRSYSSIILPVVIALIVITLSVFVLVGLYRMCWKADPGTPENGNDQPQSDKE
		* *. *. *. *.....*. **** *. *....., *** *.....*
	MM	KIATTPSTTPSYSSIILPVVIALVVITLLVFTLVGLYRICWKRDPGTPENGNDQPQSDKE
	HP	SVKLLTVKTISHESGEHSAQGKTKN
20		*****
	MM	SVKLLTVKTISHESGEHSAQGKTKN

25 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. AA486620) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10720> (SEQ ID NOS: 64, 74 and 84)

Determination of the whole base sequence of the cDNA insert of clone HP10720 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5'-untranslated region, a 669-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein consisting of 222 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,219 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 35 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Val-Thr at position 76 and Asn-His-Thr at position 93). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to

expect that the mature protein starts from glutamic acid at position 15.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792241) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP10721> (SEQ ID NOS: 65, 75 and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10721 obtained from cDNA library of human kidney revealed the structure consisting of a 74-bp 5'-untranslated region, a 552-bp ORF, and a 1658-bp 3'-untranslated region. The ORF encodes a protein consisting of 183 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat larger than the molecular weight of 19,989 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 22 kDa. Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 25.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R27187) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10725> (SEQ ID NOS: 66, 76 and 86)

Determination of the whole base sequence of the cDNA insert of clone HP10725 obtained from cDNA library of human kidney revealed the structure consisting of a 235-bp 5'-untranslated region, a 789-bp ORF, and a 713-bp 3'-untranslated region. The ORF encodes a protein consisting of 262 amino acid residues and there existed one putative transmembrane domain. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example,

Accession No. AI127782) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP10727> (SEQ ID NOS: 67, 77 and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10727 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 102-bp 5'-untranslated region, a 507-bp ORF, and a 947-
10 bp 3'-untranslated region. The ORF encodes a protein consisting of 168 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the
15 Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was larger than the molecular weight of 17,822 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa.
20 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 29.

The search of the GenBank using the base sequences
25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. R80316) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10728> (SEQ ID NOS: 68, 78 and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10728 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 221-bp 5'-untranslated region, a 732-bp ORF, and a 902-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 26,534 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H23535) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10730> (SEQ ID NOS: 69, 79 and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10730 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 27-bp 5'-untranslated region, a 1287-bp ORF, and a 1216-bp 3'-untranslated region. The ORF encodes a protein consisting of 428 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight of 48,992 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C19105) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10742> (SEQ ID NOS: 70, 80 and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10742 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 231-bp 5'-untranslated region, a 852-bp ORF, and a 828-

bp 3'-untranslated region. The ORF encodes a protein consisting of 283 amino acid residues and there existed two putative transmembrane domains. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was smaller than the molecular weight of 31,629 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T35949) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03800> (SEQ ID NOS: 91, 101 and 111)

Determination of the whole base sequence of the cDNA insert of clone HP03800 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 67-bp 5'-untranslated region, a 1431-bp ORF, and a 135-bp 3'-untranslated region. The ORF encodes a protein consisting of 476 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 55 kDa that was almost identical with the molecular weight of 54,110 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Lys-Thr at position 81, Asn-Met-Thr at position 132, Asn-Val-Thr at position 307 and Asn-Gln-Thr at position 346). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mosquito vitellogenic carboxypeptidase (Accession No. P42660). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mosquito vitellogenic carboxypeptidase (VC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.5% in the entire region. In addition, the C-terminal portion beginning from alanine at position 182 matched with

human probable carboxypeptidase (Accession No. AAC23787)
except one amino acid residue.

Table 21

5

HP MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPK-GDSGQPLFLTPYIEAGKIQKG

... * * . ** . *.**.****** ...***...

VC MVKFHLLVLIIFTCTCSDATLWNPYKKLMRGSASPPRPGESGEPLFLTPLLQDGKIEEA

10

HP RELSLVGPFPGGLNMKSYAGFLTVNKTYSNLFWFPPAQIQPEDAPVVLWLQGGPGGSSM

*. . *.. ...**.***.*. ..*****. **. ...*.*...*****. **.

VC RNKARVNHMLSSVESYSGFMTVDAKHNSNLFWFYVPAKNNREQAPILVWLQGGPGASSL

HP FGLFVEHGPYVVTSNMTLRDRDFPWTTLTMLYIDNPVGTGFSFTDDTHGYAVNEDDVAR

15

..**..*.....*...* . *.*****.....**..**..*.

VC FGMFEENGPFHIHRNKSQREYSWHQNHMIYIDNPVGTGFSFTDSDEGYSTNEEHVGE

HP DLYSALIQFFQIFPEYKNDFYVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGD

. * . . *** .**.. ..**..****.***.*... ** *. ..****.*.****

20

VC NLMKFIQQFFVLFPNLLKHPFYISGESYGGKFVPAFGYAIH-NSQSQPKINLQGLAIGD

HP GYSDPESIIGGYAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGD

. . . *.**.***.* . * *... . *. * ... *.**

VC GYTDPLNQL-NYGEYLYELGLIDLNGRKKFDEDTAAAIACAERKDMNSANRLIQGLFDG-

25

human kidney revealed the structure consisting of a 191-bp 5'-untranslated region, a 681-bp ORF, and a 223-bp 3'-untranslated region. The ORF encodes a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human claudin-10 (Accession No. NP_008915). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human claudin-10 (CD). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 76.2% in the entire region. The C-terminal region downstream from glycine at position 72 completely matched with that sequence.

Table 22

120

HP MSRAQIWALVSGVGGFGALVAATTSNEWKVTTTRASSVITATWVYQGLWMNCAGNALGS

..* *.. ...* ***.* ...***. . . **..*... *

CD MASTASEIIAFMVISGWVLSSTLPTDYWKVSTIDGTVITTATYWANLWKACVTDSTGV

5 HP FHCRPHFTIFKVAGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

.*.*****

CD SNCKDFPSMLALDGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

HP GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

10 *****

CD GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

HP FSISDNNKTPRYTYNGATSVMSRRTKYHGGEDFKTTNPSKQFDKNAYV

15 CD FSISDNNKTPRYTYNGATSVMSRRTKYHGGEDFKTTNPSKQFDKNAYV

Furthermore, the search of the GenBank using the
base sequences of the present cDNA has revealed the
20 registration of sequences that shared a homology of 90% or
more (for example, Accession No. N41613) among ESTs. However,
since they are partial sequences, it can not be judged
whether or not they encode the same protein as the protein
of the present invention.

25 <HP03879> (SEQ ID NOS: 93, 103 and 113)

Determination of the whole base sequence of the cDNA insert of clone HP03879 obtained from cDNA library of human kidney revealed the structure consisting of a 33-bp 5'-untranslated region, a 918-bp ORF, and a 651-bp 3'-untranslated region. The ORF encodes a protein consisting of 305 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was almost identical with the molecular weight of 34,073 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human NADH-cytochrome b5 reductase (Accession No. Y09501). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human NADH-cytochrome b5 reductase (CT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 63.5% in the entire region other than the N-terminal region.

Table 23

	HP	MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHN
		* . ** * . ** * . * . ** ** * ** .
5	CT	MGAQLSTLGHMVLFPVWFLYSLLMKLFQRS-TPAITLESPDIKYPLRLIDREIISHD
	HP	TKRFRFALPTAHHTLGLPVGKHIYLSRIDGSLVIRPYTPVTSDEDQGYVDLVIKYYLKG
		* . ***** . . * . ***** . ***** . **** . ** . ***** . ** . * . * . ***** . *
	CT	TRRFRFALPSPQHILGLPVGQHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKYYFKD
10	HP	VHPKFPEGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGFNIQPNKKSPEPRVAKKLG
		. ***** . ***** . * . . ** . ***** . * **** . * . * . *** * * . . . *
	CT	THPKFPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKKSNIIRT VKSVG
15	HP	MIAGGTGITPMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
		***** . ***** . **** . * * . * * ***** . ** . **** *****
	CT	MIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNKHSARFKLW
	HP	FTLDHPPKDWAYSKGFVTADMIREHLPAGDDVLVLLCGPPPMVQLACHPNLDKLGYSQK
20		. *** . * . * . * . *** . . *** . *** . * . . *** . ***** . * ** ***** . * . . .
	CT	YTLDRAPAWDYGGGFVNEEMIRDHLPPPEEEPLVLMCGPPPMIQYACLPNLDHVGHPT
	HP	MRFTY
		. * .
25	CT	RCFVF

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F06459) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP03880> (SEQ ID NOS: 94, 104 and 114)

Determination of the whole base sequence of the cDNA insert of clone HP03880 obtained from cDNA library of human kidney revealed the structure consisting of a 98-bp 5'-untranslated region, a 684-bp ORF, and a 115-bp 3'-untranslated region. The ORF encodes a protein consisting of 227 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,717 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 27 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to

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20

25

expect that the mature protein starts from aspartic acid at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat phosphatidylethanolamine-binding protein (Accession No. P31044). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat phosphatidylethanolamine-binding protein (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the region of 133 amino acid residues other than the N-terminal region.

Table 24

20	HP MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV
	RN MAADISQWAGPLSLQEVEPPQHALRVDYGGVTV
	HP VPDCCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG
	... * * *.**..***** .*. * *.**..**
25	RN DELGKVLTPQVMNRPSSISWDGLDPGKLYTLVLTDPDAPSRKDPKFREWHHFLVVMKG

HP ADLKKGKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKV---ISLLP-KENKTRGSWK
 .*.***. **.* ...** ..*.*** ...** ***. *....***.*
 RN NDISSGTV---LSEYVCGSGPPKDTGLHRYVWLVEEQEQLNCDEPILSNKSGDNRGKFK

5

HP MDRFLNRFHLGPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC
 ...* ...***.* *.* **.*.
 RN VESFRKKYHLGAPVAGTCFQAEWDDSVPKLHDQLAGK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H83784) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10704> (SEQ ID NOS: 95, 105 and 115)

Determination of the whole base sequence of the cDNA insert of clone HP10704 obtained from cDNA library of human kidney revealed the structure consisting of a 141-bp 5'-untranslated region, a 1326-bp ORF, and a 399-bp 3'-untranslated region. The ORF encodes a protein consisting of 441 amino acid residues and there existed eight putative transmembrane domains. Figure 35 depicts the

25

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human unknown gene product (Accession No. AAC27544). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention
10 (HP) and human unknown gene product (UP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins
15 shared a homology of 39.1% in the entire region.

Table 25

HP	MAIHKALVMCLGLPLFLFPG-AWAQGHVPPGCSQGLNPLYYNLCDRSGAWGIVLE
20	* **.... * ... **..* * * .*** .. ****.*
UN	MFVASERKMRAHQVLTFLLLFVITSVASENASTSRGCGDLLPQYVSLCDLDAIWGIVVE
HP	AVAGAGIVTTFVLTIIILVASLPFVQDTKKRSLTQVFFLLGTLGLFCLVFACVVKPDFS
	***** ..*.* **...***.....*.* * . ***** *.* ... * .
25	UN AVAGAGALITLLMLILLVRLPFIKEKEKKSPVGLHFLFLLGTLGLFGLTFAFIQEDET

HP TCASRRFLFGVLFALCFSCLAHVFLARNHGPGRGWVIFTVALLTLVEVIINTEW
*. ****.*****.***** *.**.. ** ** ..** * **.***..**
UN ICSVRRFLWGVLFALCFSCLLSQAWRVRLVRHGTGPAGWQLVGLALCLMLVQVIIAVEW

5
HP LIITLVRGSGEGGPQGNSSAGWAVASPCAIANMDFVMALIYVMLLLLGAFLGAWPALCGR
....*** . ***** *.**.. * .***.
UN LVLTVLR-----DT-----RPACAYEPMDFVMALIYDMVLLVVTGLALFTLCGK

10
HP YKRWRKHGVFVLLTTATSVAIWVWVIMYTYGN-KQHNSPTWDDPTLAIALAANAWAFVL
.***..*.*.*.*. ** ***.**..**..** * ... *.*****.***..*.*.
UN FKRWKLNGAFLLITAFLSVLIWVAWMTMYLFGNVKLQQGDAWNDPTLAITLAASGWVFI

15
HP FYVIPEVSQVTKSSPEQSYQGDMYPTRGVGY-ETILKEQ-KGQSMFVENKAFSMDEPVAA
*..***. . * .. *. . . *. ** ..*. . . .*****. **
UN FHAIPEI-HCTLLPALQENTPNYFDTSQPRMRETAFEEDVQLPRAYMENKAFSMDEHNAA

HP KRPVS-PYSGYNGQLLTSVYQPTMALMHKVPSEGAYDIILPRATANSQVMGSANSTLRA
*... * .. . *. * . . . * . * *.
20
UN LRTAGFPNGSLGKRPSGLGKRPSAPFRSNVYQPTEMAVVLNGGTIPTAPPSHTGRHLW

HP EDMYSAQSHQAATPPKDGKNSQVFRNPYVWD

of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA346702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
5 encode the same protein as the protein of the present invention.

<HP10715> (SEQ ID NOS: 96, 106 and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10715 obtained from cDNA library of
10 human umbilical cord blood revealed the structure consisting of a 49-bp 5'-untranslated region, a 798-bp ORF, and a 1351-bp 3'-untranslated region. The ORF encodes a protein consisting of 265 amino acid residues and there existed two putative transmembrane domains. Figure 36 depicts the
15 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was larger than the molecular weight of 29,217 predicted from the ORF.

20 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI381750) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
25 encode the same protein as the protein of the present

invention.

<HP10724> (SEQ ID NOS: 97, 107 and 117)

Determination of the whole base sequence of the cDNA insert of clone HP10724 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 68-bp 5'-untranslated region, a 627-bp ORF, and a 1485-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was almost identical with the molecular weight of 23,850 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T78035) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10733> (SEQ ID NOS: 98, 108 and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10733 obtained from cDNA library of human umbilical cord blood revealed the structure consisting

of a 102-bp 5'-untranslated region, a 1203-bp ORF, and a 222-bp 3'-untranslated region. The ORF encodes a protein consisting of 400 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was larger than the molecular weight of 43,151 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Leu-Thr at position 52, Asn-Ala-Ser at position 131, Asn-Ile-Thr at position 145 and Asn-Leu-Ser at position 343). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from arginine at position 33.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH protein (Accession No. Q06003). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Drosophila melanogaster*

GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.0% in the entire region.

Table 26

10 HP MAWRRREASVGARGVLALALLALALCVPGARGRALEWFSAVVNIEYVDPQTNLTVWSVSE

HP SGRFGDSSPKEGAHGLVGVPWAPGGDLEGCAPDTRFFVPEPGGRGAAPWVALVARGGCTF

HP KDKVLVAARRNASAVVLYNEERYGNITLPM SHAGTGNIVVIMISYPKGREILEL-VQKGI

15 * *... ..*.*. .*. *...*

DM MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGY

HP PVTMTIGVGTRHVQEF--ISGQSVVFVAIAFITMMIISLAWLIFYYIQRFLY-TGSQIGS

.* * * *... .. **. **. *. ** . * *** * ... *

20 DM NVTISIIIEGRRGVRTISSLNRTSVLFVSISFI--VDDILCWLIFYYIQRFRYMQAKDQQS

HP QSHRKETKKVIGQLLLHTVKHGEKGIDVDAENCAVCIENFKVKDIIRILPCKHIFHRICI

.. . ***.* .. * * .. . *. *. **. ***. * *. ***** **.

DM RNLCSVTKKAIMKIPTKTGKFS-DKDLSDCCAICIEAYKPTDTIRILPCKHEFHKNCI

25

HP DPWLLDHRTCPMCKLDVIKALGYWGEPGDVQEMPAPESPPGRDPAANLSLALPDDGSDDE

*****.*****.* ** *. *

DM DPWLVIEHRTCPMCKLDVLKFYGY-VVGDQIYQTPSPQHTAPIASIEEVPVIVVAVPHGPQ

5 HP SSPPSASPAESEPQCPSFKGDAGENTALLEAGRSDSRHGGPIS

. . * . . . * . . . *

DM PLQPLQASNMSSFAPSHYFQSSRSPSSSVQQQLAPLTYQHPQQAASERGRRNSAPATMP

10 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AI286184) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
15 encode the same protein as the protein of the present
invention.

<HP10734> (SEQ ID NOS: 99, 109 and 119)

Determination of the whole base sequence of the
cDNA insert of clone HP10734 obtained from cDNA library of
20 human umbilical cord blood revealed the structure consisting
of a 124-bp 5'-untranslated region, a 579-bp ORF, and a
1202-bp 3'-untranslated region. The ORF encodes a protein
consisting of 192 amino acid residues and there existed one
putative transmembrane domain. Figure 39 depicts the
25 hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human sodium channel $\beta 2$ subunit (Accession No. AAD47196). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human sodium channel $\beta 2$ subunit (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 26.3% in the N-terminal region of 152 amino acid residues.

Table 27

HP	MFCPLKLILLPVLLDYSGLNDLNVS-PPELTVHVGDSALMGCVFQS--TEDK
20	...*. *.....*. *.*.* *.*. *.*.* *..
SC	MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTPATLNVLNGSDARLPCTFNSCYTVNH
HP	CIFKIDWTLSPGEHAKDE-YVLYYYSNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQEA
	*...** .. .****.**.. *. * *..*..** .
25	SC KQFSLNWTYQECNNCSEEMFLQFRMKIINLKLRFQDRVEFSGNPSKYDVSVMRLRNVQPE

HP DQGTICEIRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVE

..*.*.**.*** ** * *. ..

SC DEGIYNCYIMNPPDRHRGHGKIHLQVLMEEPPERDFTVAVIVGASVGGFLAVVILVMVV

5

HP WIFSGRRRAKVTRRKHHCVREGSG

SC KCVRRKKEQKLSTDDLKTEEEGKTDGEGNPDDGAK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C03216) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

15

<HP10756> (SEQ ID NOS: 100, 110 and 120)

20

Determination of the whole base sequence of the cDNA insert of clone HP10756 obtained from cDNA library of human kidney revealed the structure consisting of a 49-bp 5'-untranslated region, a 783-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 260 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 40 depicts the

25

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,356 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW027769) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03670> (SEQ ID NOS: 121, 131 and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03670 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 77-bp 5'-untranslated region, a 1014-bp ORF, and a 531-bp 3'-untranslated region. The ORF encodes a protein consisting of 337 amino acid residues and there existed at least seven putative transmembrane domains. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein KIAA0260

(Accession No. BAA13390). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein KIAA0260 (KI). Therein, the marks of -, *, and . represent

5 a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 57.6% in the entire region other than the N-terminal region. In

10 addition, the C-terminal region beginning from leucine at position 77 matched with human putative Sqv-7-like protein (Accession No. AJ005866) except one amino acid residue.

Table 28

15

HP MTAGGQAEAEAGAGGEPG

KI NSWSPLGAAAAGPRAARPRRQATAAAAAAMAEVHRRQHARVKGEAPAKSSTLRDEEELGMA

20 HP AARLPSRVARLLSALFYGTCSFLIVLVNKALLTTYGFPSPIFLGIGQMAATIMILYVSKL

. **.* **.*.*****.***.***.* **.*. .*.***.***. .*.***

KI SAETLTVFLKLLAAGFYGVSSFLIVVVNKSVL TNYRFPSSLCVGLGQMVATVAVLWVGKA

HP NKIIHFPDFDKKIPVKLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLLLETI

25***.*...* * ***** **.*** **.*.*****.*.*.*..*..

KI LRVVKFPDLDRNVPRKTFPLPLLYFGNQITGLFSTKKLNLPMFTVLRRFSILFTMFAEGV

HP ILGKQYSLNIILSVFAIILGAFIAAGSDLA FNLEGIYIFVFLNDIFTAANGVYTKQKMDPK

. * * . * . * .. ***. *. ***. **. *****. **** *... **.. *****. *. ***. *. *

5 KI LLKKTFSWGIKMTVFAMIIGAFVAASSDLAFDLEGYAFILINDVLTAAANGAYVKQKLDISK

HP ELGKYGVLFYNACFMIIPTLIISVSTGDLQQATEFNQWKNVVFILQFLLSCFLGFLMYS

*****. *. *** ***. *** *. *** *. *. **. * ... *. *** *** **. ***.

KI ELGKYGLLYNALFMILPTLAIAYFTGDAQKAVEFEGWADTLFLLQFTLSCVMGFILMYA

10

HP TVLCSYNSALTTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRYSFLTL

****. *****. ** ***. .. ***... *****. **. *****. **. * **.. *

KI TVLCTQYNSALTTTIVGCIKNILITYIGMVFGGDYIFTWTNFI GLNISIAGSLVYSYITF

15 HP SSQKPKPVGEENICLDLKS

... .*. *. * **. *

KI TEEQLSKQ-SEANNKLDIKGKGA

20

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R24922) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present

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invention.

<HP03688> (SEQ ID NOS: 122, 132 and 142)

Determination of the whole base sequence of the cDNA insert of clone HP03688 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 35-bp 5'-untranslated region, a 711-bp ORF, and a 1729-bp 3'-untranslated region. The ORF encodes a protein consisting of 236 amino acid residues and there existed five putative transmembrane domains. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein W02D9 (Accession No. CAB03470). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein W02D9 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.8% in the entire region other than the N-terminal

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T51465) among ESTs. However, 5 since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03825> (SEQ ID NOS: 123, 133 and 143)

Determination of the whole base sequence of the 10 cDNA insert of clone HP03825 obtained from cDNA library of human kidney revealed the structure consisting of a 20-bp 5'-untranslated region, a 1683-bp ORF, and a 36-bp 3'-untranslated region. The ORF encodes a protein consisting of 560 amino acid residues and there existed seven putative 15 transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 56 kDa that was smaller than the molecular weight of 20 64,047 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Mycobacterium tuberculosis hypothetical protein Rv0235c (Accession No. CAB07001). 25 Table 30 shows the comparison between amino acid sequences

of the human protein of the present invention (HP) and Mycobacterium tuberculosis hypothetical protein Rv0235c (MT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the entire region other than the N-terminal region. In addition, the region from alanine at position 293 to proline at position 502 matched with human putative novel protein c360B4.1 (Accession No. CAB56180).

Table 30

15	HP MAAPAESLRRRKTYSDPEPESPPAPGRGPAGSPAHLHTGTFWLTRIVLLKALAFVYFVA	
		. . . **. * . * . . * . * . *
	MT	MGWFSAP EYWLGR LALERGTAI IYLIA
	HP FLVAFHQNKQLIGDRGLLPCRVLKQYFQDRTSWEVFSYMP TILW LMDWSDMNSNLD	
20	* . * . * . . * . * . * . * * . * . . . * . . . *	
	MT FVAAAQQFRPLIGEHGMLPVPRYLAG-QSFWRTPSIFH-FRYS DRV FAGVCW—LGAVLS	
	HP LLALLGLGISSFVLITGCANMLLMAALWGLYMSLVNVGHVWYSFGWESQLLETGFLGIFL	
	* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *	
25	MT —AAVAGAASFVPLW—ATMLIWLTLWVLYLSIVNVGQAWYSFGWESLLETGFLMIFL	

HP SLEELRPYFRDRGWPLPGPL

** ..

MT SLRKVASPPAD

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA019047) among ESTs. However, since they are
10 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03877> (SEQ ID NOS: 124, 134 and 144)

Determination of the whole base sequence of the
15 cDNA insert of clone HP03877 obtained from cDNA library of human kidney revealed the structure consisting of a 106-bp 5'-untranslated region, a 1221-bp ORF, and a 678-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed four putative
20 transmembrane domains. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 49 kDa that was somewhat larger than the molecular weight
25 of 46,208 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein Y37D8A (Accession No. CAA21543). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein Y37D8A (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.2% in the intermediate region of 329 amino acid residues.

Table 31

HP	MAENG
CE	MAKKQKKSTSEKERTVEFKEPPK PANSEERLVSTRQFLAKIGQKKLIK KKVKNFRFSKKT
HP	KNCDQRRVAMNKEHHNGNFTDPSSVNEKKRREREERQNI VLWRQPLITLQYFSLEILVIL
	. * ** . ** . ** . * * . . * . ** .
CE	FIDFFSENQKKNCRLKPAGRGMKPSPSQNTLNRMERETIVFWRRPHIVIPYALMEIAHLA
HP	KEWTSKLWHRQSIVVSFLLLLAVLIATYYVEGVHQYVQRIEQFLLYAYWIGLGILSSV

[illegible]

25

The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T18977) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
5 encode the same protein as the protein of the present invention.

<HP10765> (SEQ ID NOS: 125, 135 and 145)

Determination of the whole base sequence of the cDNA insert of clone HP10765 obtained from cDNA library of
10 human umbilical cord blood revealed the structure consisting of a 30-bp 5'-untranslated region, a 1362-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 453 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative
15 transmembrane domain in the inner portion. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 48 kDa that was almost identical with the molecular
20 weight of 47,724 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792834) among ESTs. However, since they are
25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10766> (SEQ ID NOS: 126, 136 and 146)

Determination of the whole base sequence of the
5 cDNA insert of clone HP10766 obtained from cDNA library of
human kidney revealed the structure consisting of a 150-bp
5'-untranslated region, a 180-bp ORF, and a 675-bp 3'-
untranslated region. The ORF encodes a protein consisting of
59 amino acid residues and there existed two putative
10 transmembrane domains. Figure 46 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 10 kDa or less that was almost identical with the
15 molecular weight of 6,098 predicted from the ORF.

The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. T85491) among ESTs. However, since they are
20 partial sequences, it can not be judged whether or not they
encode the same protein as the protein of the present
invention.

<HP10770> (SEQ ID NOS: 127, 137 and 147)

Determination of the whole base sequence of the
25 cDNA insert of clone HP10770 obtained from cDNA library of

human kidney revealed the structure consisting of a 150-bp 5'-untranslated region, a 633-bp ORF, and a 186-bp 3'-untranslated region. The ORF encodes a protein consisting of 210 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was larger than the molecular weight of 22,156 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792771) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10772> (SEQ ID NOS: 128, 138 and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10772 obtained from cDNA library of human kidney revealed the structure consisting of a 19-bp 5'-untranslated region, a 498-bp ORF, and a 724-bp 3'-untranslated region. The ORF encodes a protein consisting of 165 amino acid residues and there existed four putative transmembrane domains. Figure 48 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F11871) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
10 encode the same protein as the protein of the present invention.

 <HP10773> (SEQ ID NOS: 129, 139 and 149)

 Determination of the whole base sequence of the cDNA insert of clone HP10773 obtained from cDNA library of
15 human kidney revealed the structure consisting of a 186-bp 5'-untranslated region, a 489-bp ORF, and a 499-bp 3'-untranslated region. The ORF encodes a protein consisting of 162 amino acid residues and there existed four putative transmembrane domains. Figure 49 depicts the
20 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

 The search of the GenBank using the base sequences
25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. N33828) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10776> (SEQ ID NOS: 130, 140 and 150) .

Determination of the whole base sequence of the cDNA insert of clone HP10776 obtained from cDNA library of human kidney revealed the structure consisting of a 207-bp 5'-untranslated region, a 666-bp ORF, and a 139-bp 3'-untranslated region. The ORF encodes a protein consisting of 221 amino acid residues and there existed three putative transmembrane domains. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 24,883 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI929639) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs and eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for expressing these proteins in large quantities. Cells into which these genes are introduced to express these proteins can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibody of the present invention can be utilized for the detection, quantification, purification and the like of the protein of the present invention.

The present invention also provides genes

corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include
5 contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements.

10 The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate
15 genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified
20 expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and
25 Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254;

Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination,

preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are
5 incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development
10 of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such
15 forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known
20 techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and
25 most preferably at least 75%) of the length of a disclosed

protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is,

naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

5 The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

 The present invention also includes polynucleotides capable of hybridizing under reduced
10 stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for
15 example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 32

Stringency Condition	Poly-nucleotide Hybrid	Hybrid Length (bp) ¹	Hybridization Temperature and Buffer ¹	Wash Temperature and Buffer ¹
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_b - T_r : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6(log₁₀[Na⁺]) + 0.41 (%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

10 Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more
15 preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and
20 identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid
sequence selected from the group consisting of SEQ ID NOS: 1
5 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

2. An isolated DNA encoding the protein according to
Claim 1.

3. An isolated cDNA comprising any one of a base
sequence selected from the group consisting of SEQ ID NOS:
10 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140.

4. The cDNA according to Claim 3 consisting of any
one of a base sequence selected from the group consisting of
SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141
to 150.

15 5. An expression vector that is capable of expressing
the DNA according to any one of Claim 2 to Claim 4 by in
vitro translation or in eukaryotic cells.

6. A transformed eukaryotic cell that is capable of
expressing the DNA according to any one of Claim 2 to Claim
20 4 and of producing the protein according to Claim 1.

7. An antibody directed to the protein according to
Claim 1.

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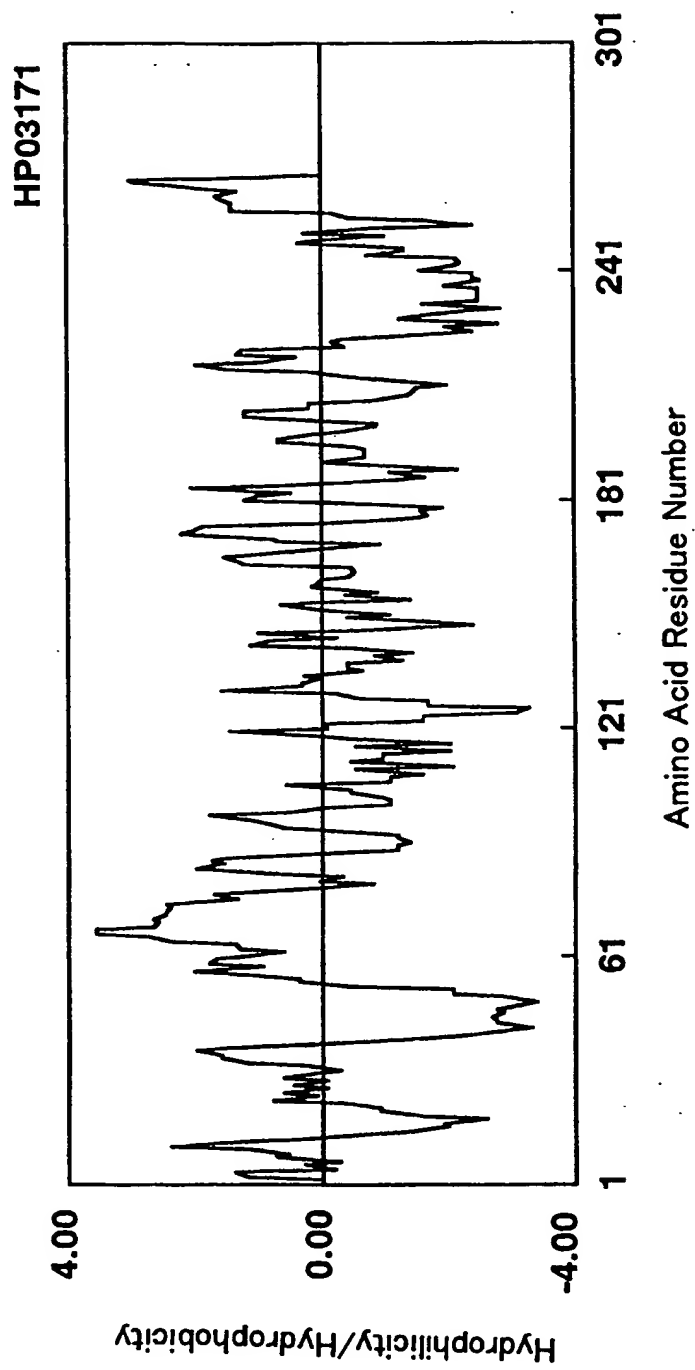


Fig.1

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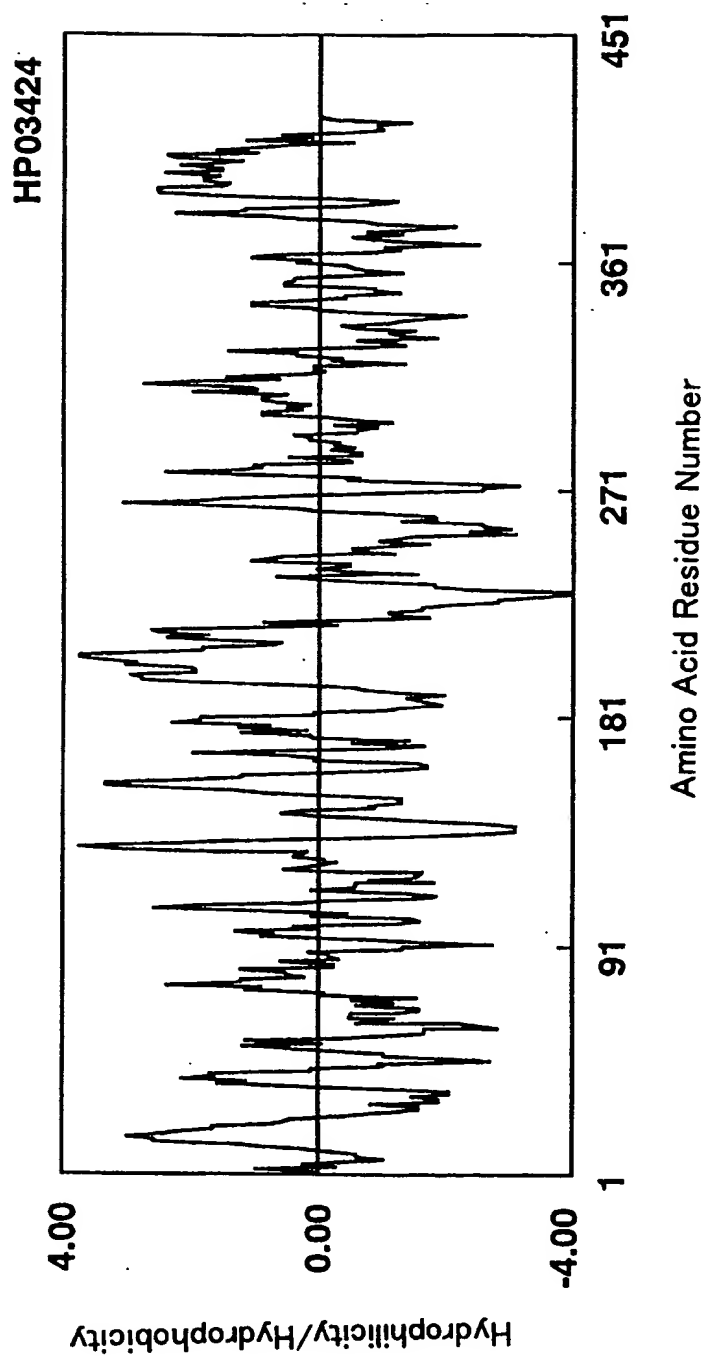


Fig.2

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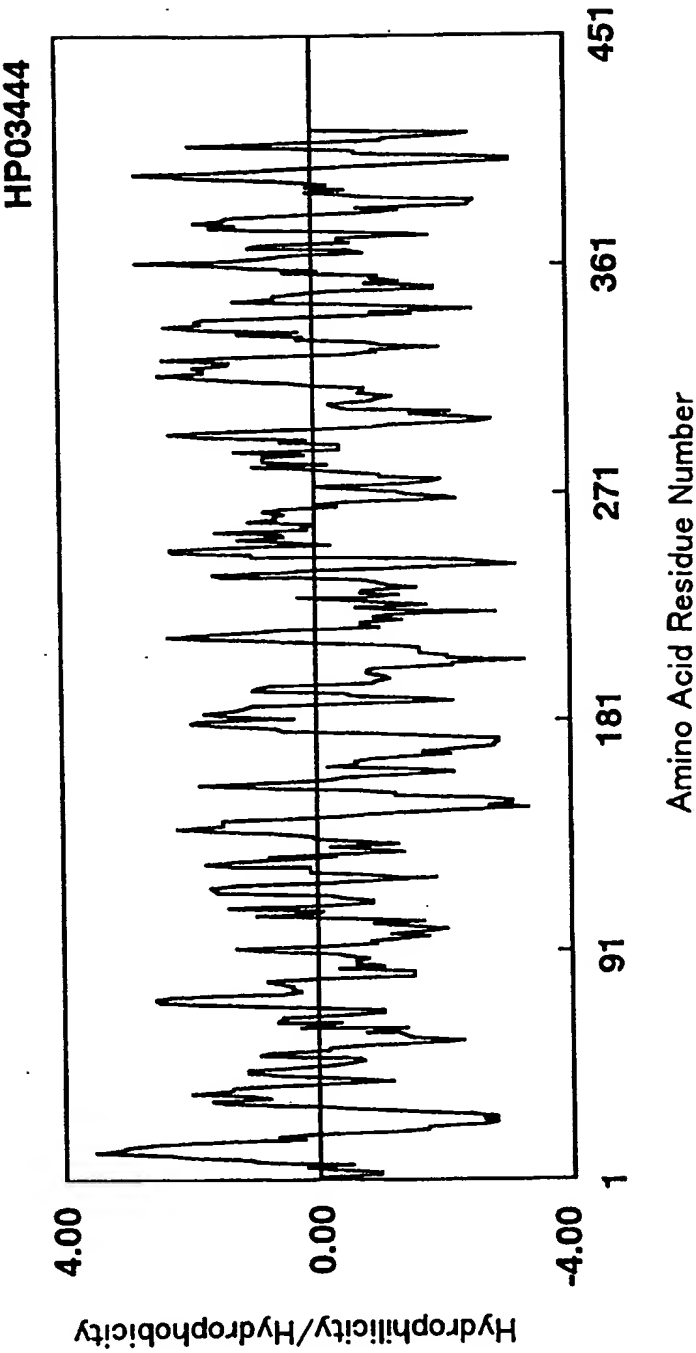


Fig.3

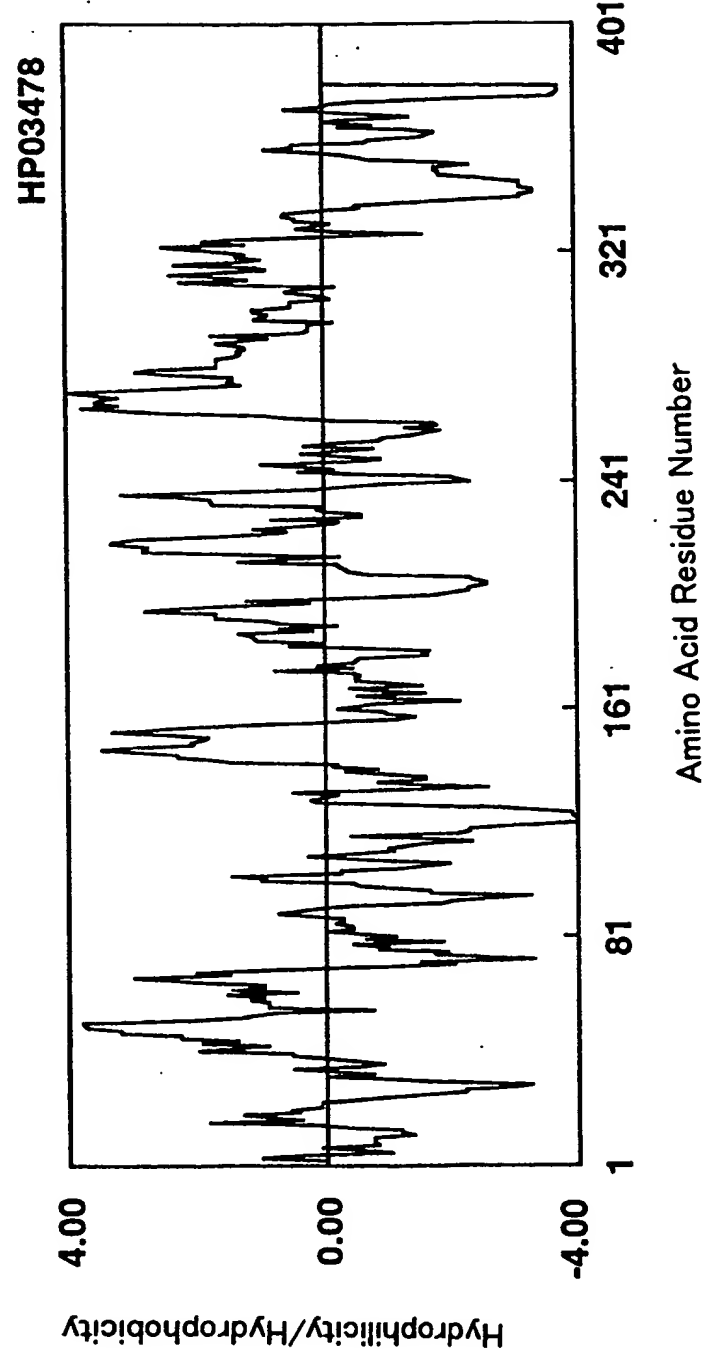


Fig.4

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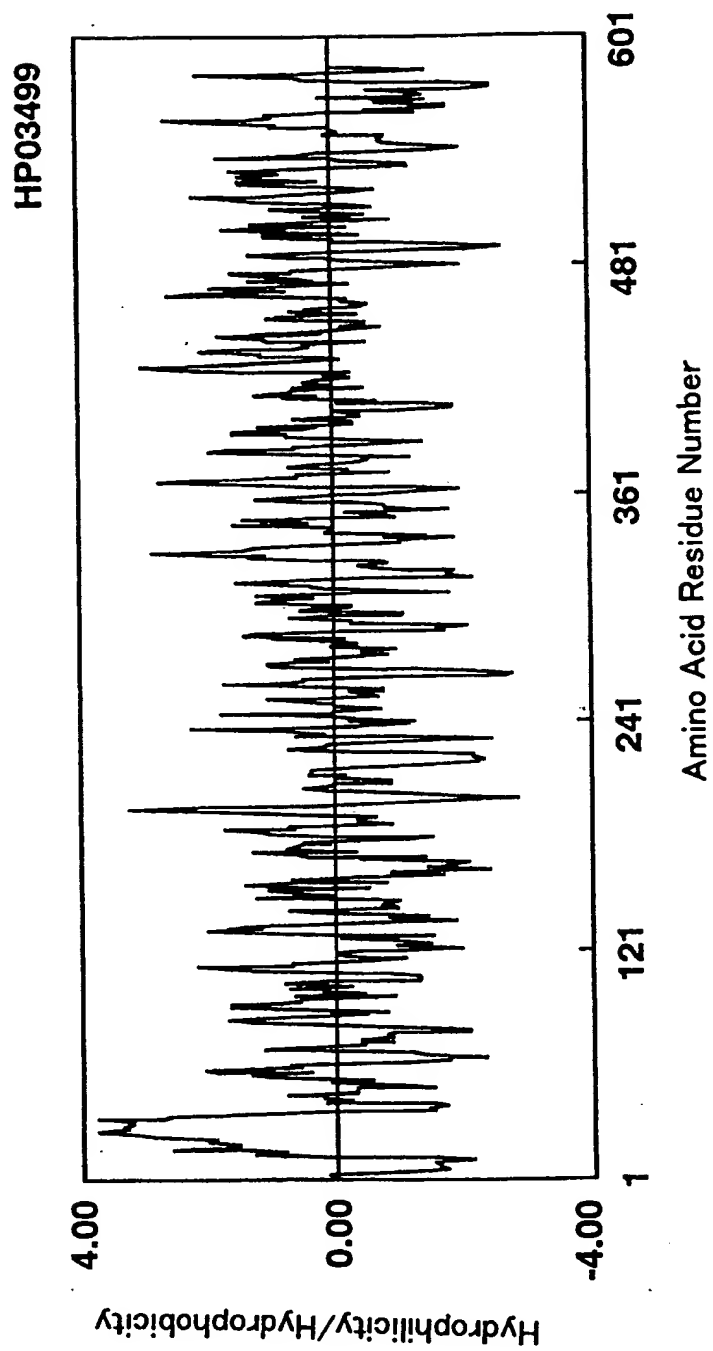


Fig.5

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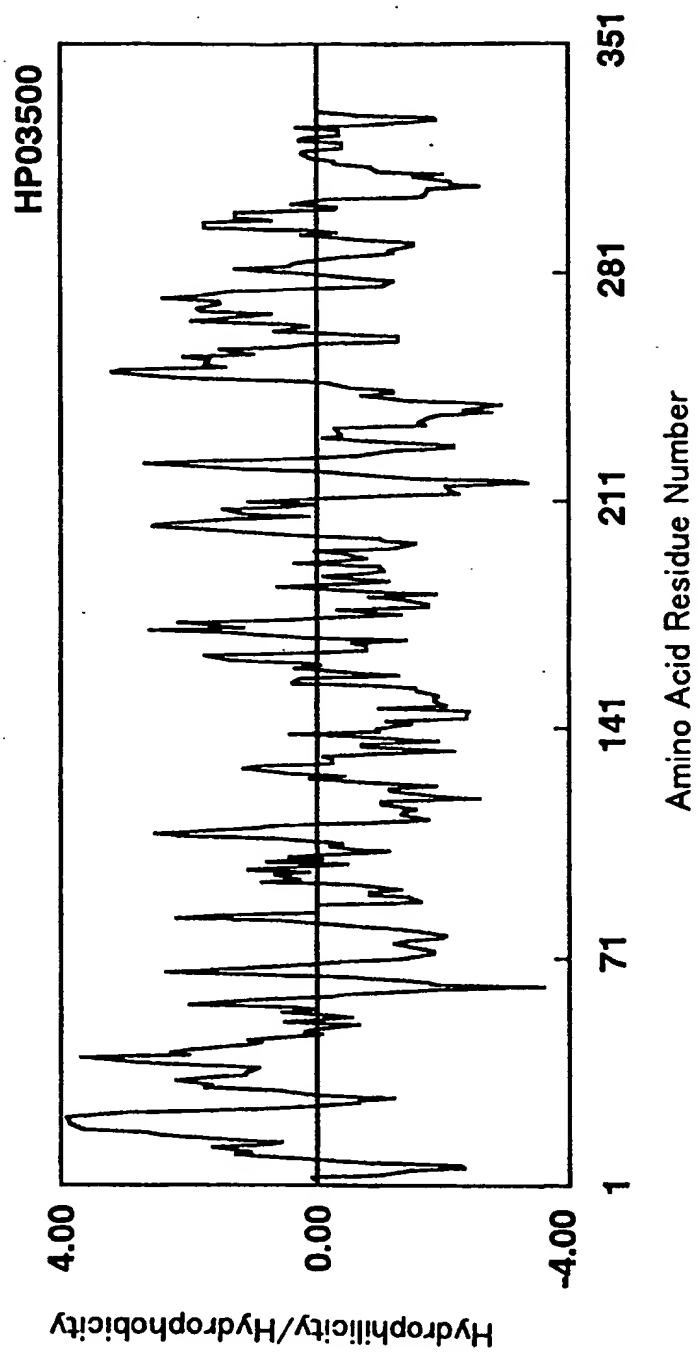


Fig.6

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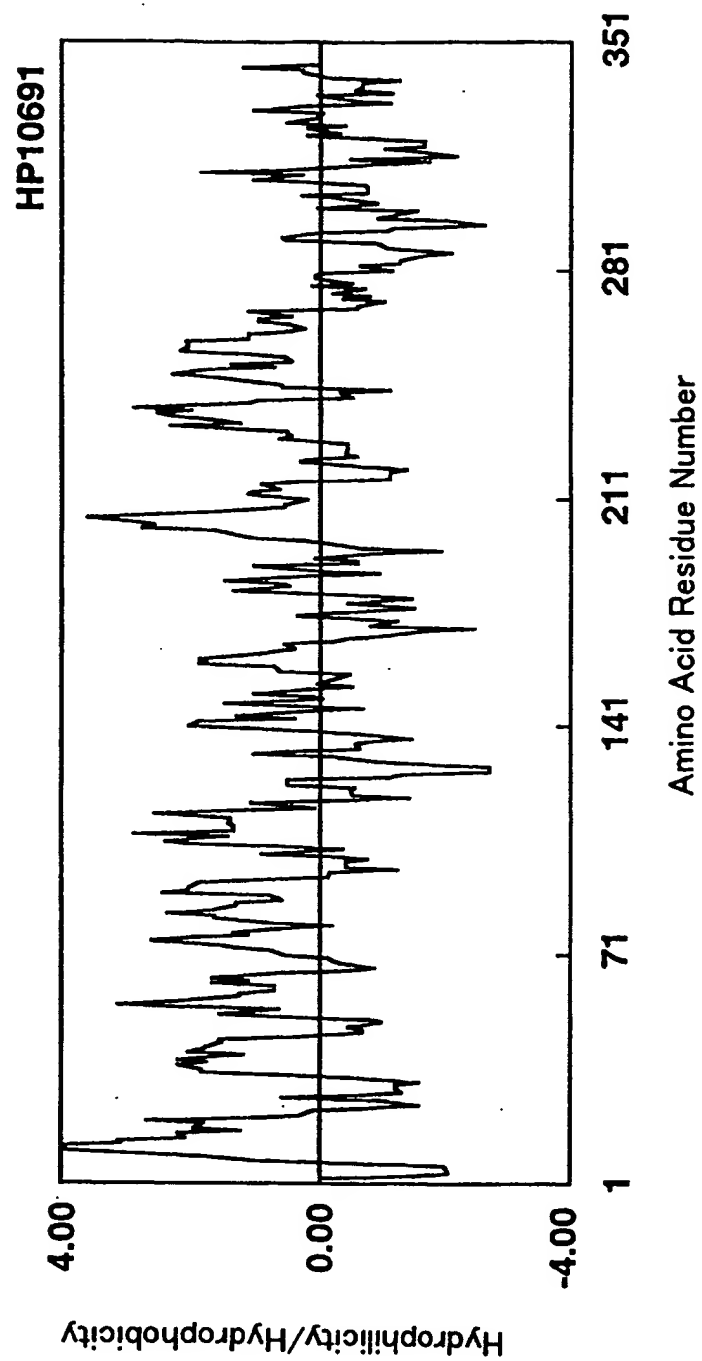


Fig.7

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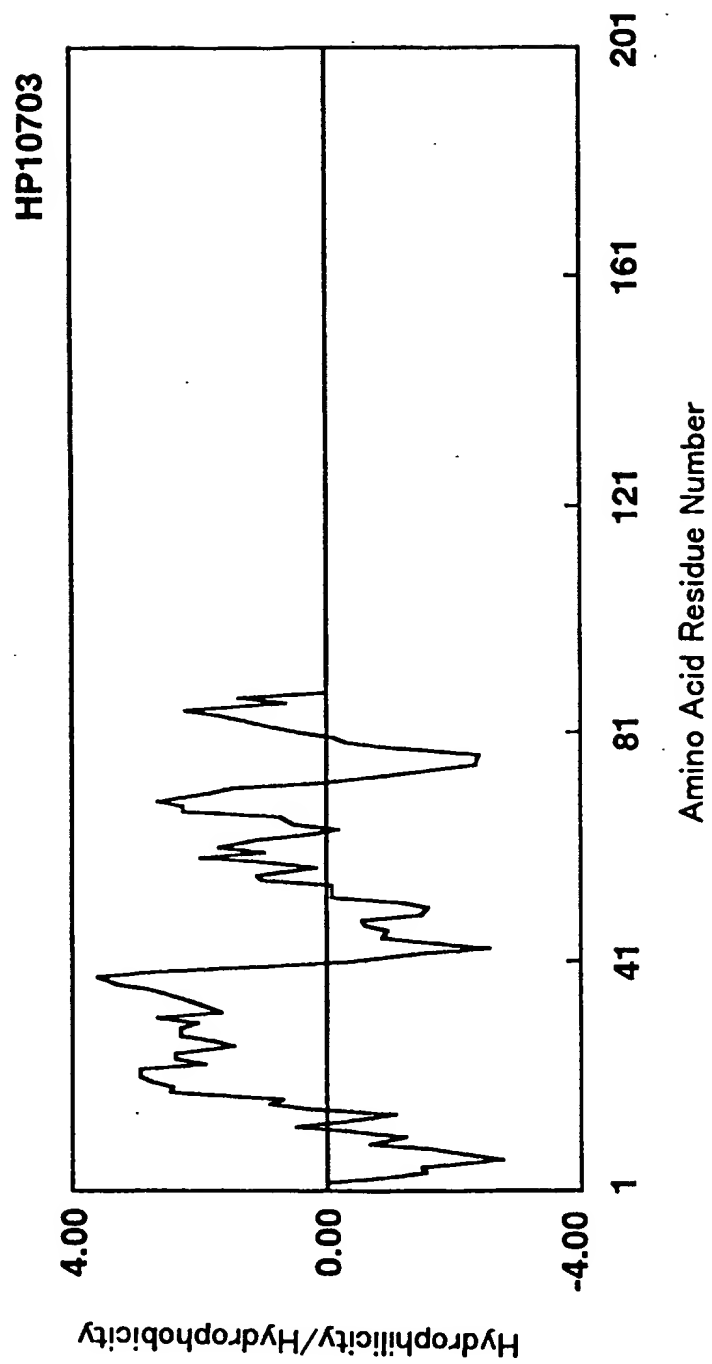


Fig.8

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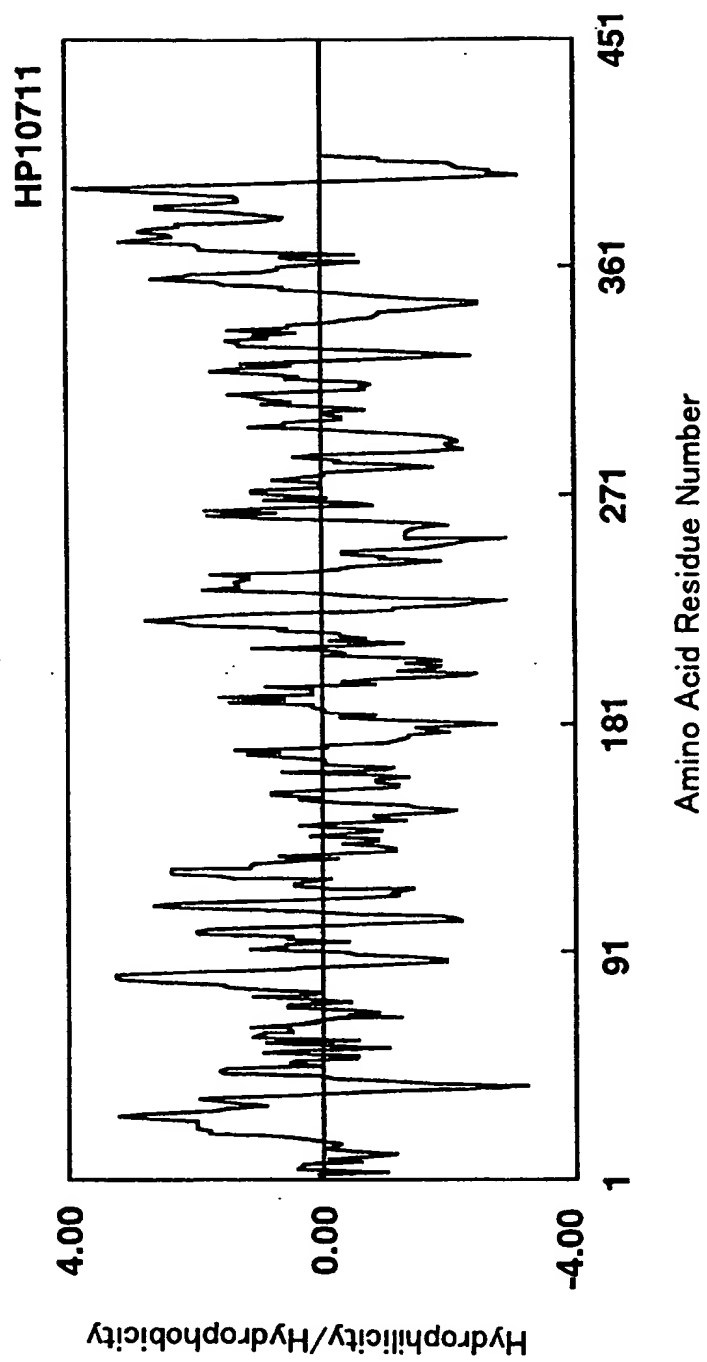


Fig.9

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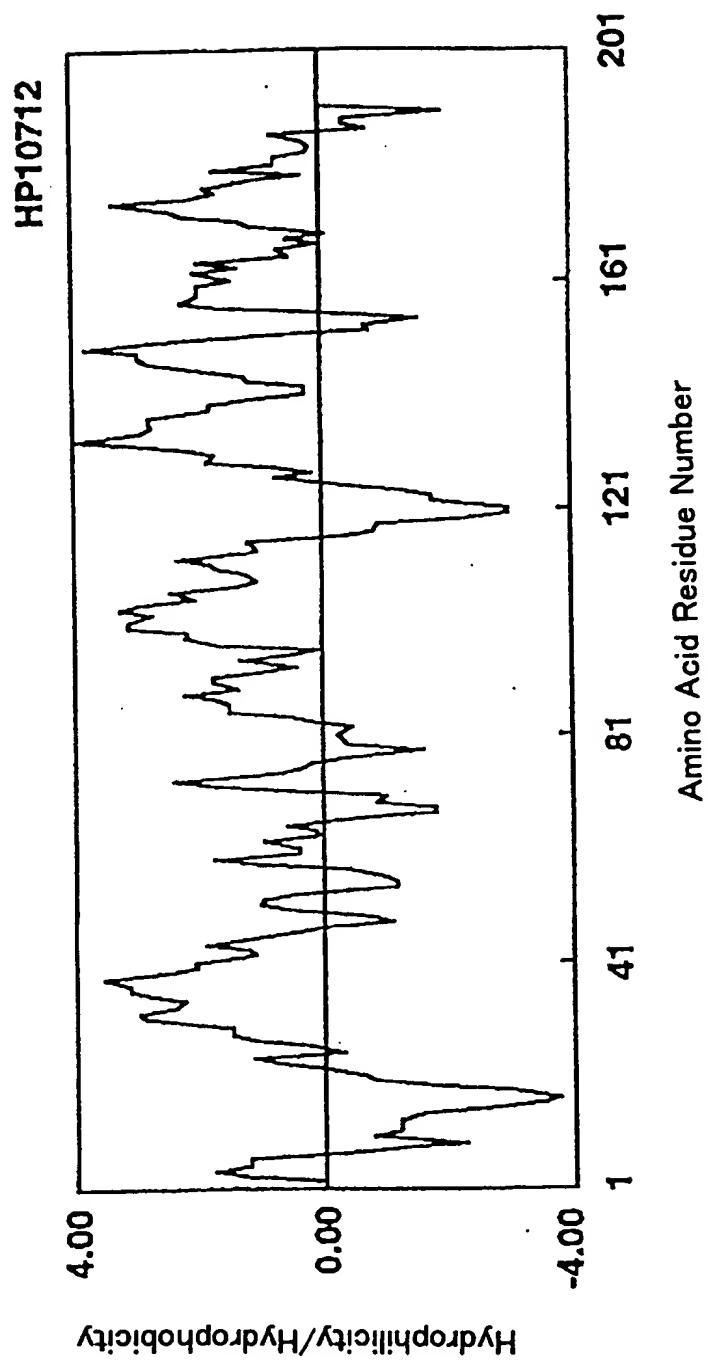


Fig.10

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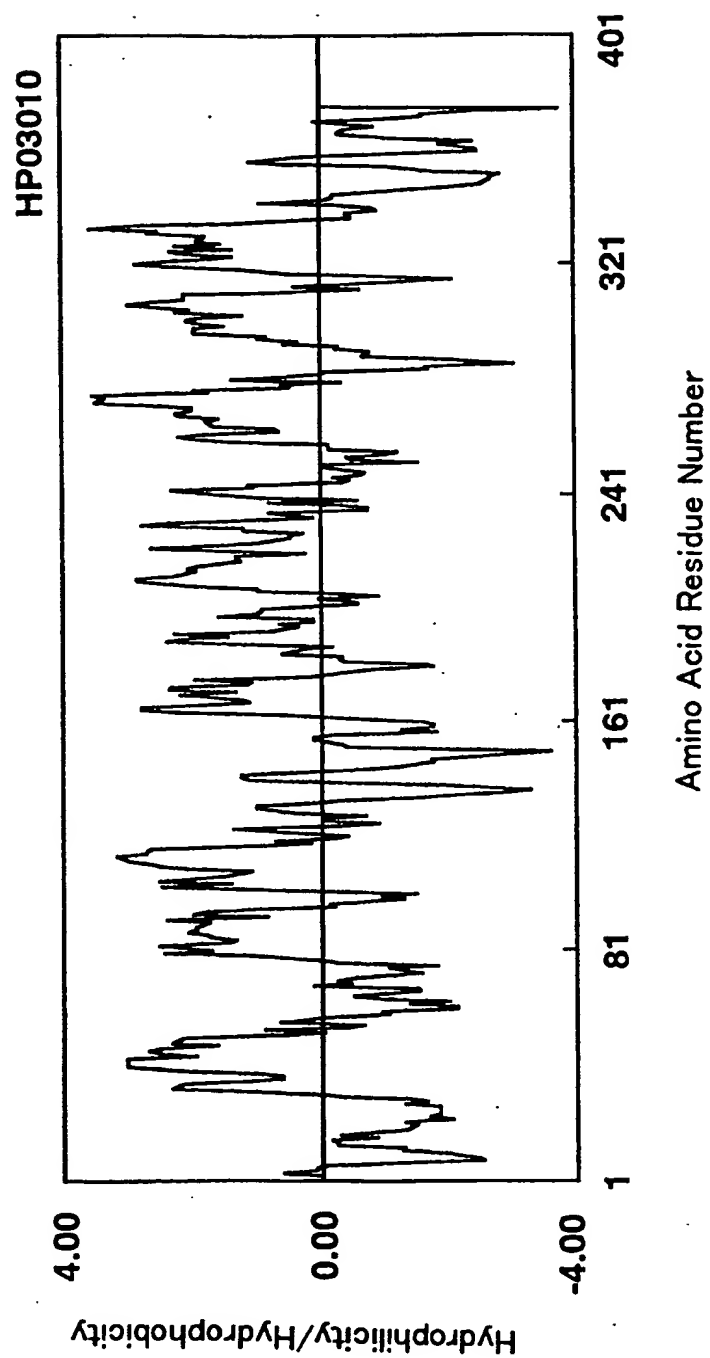


Fig.11

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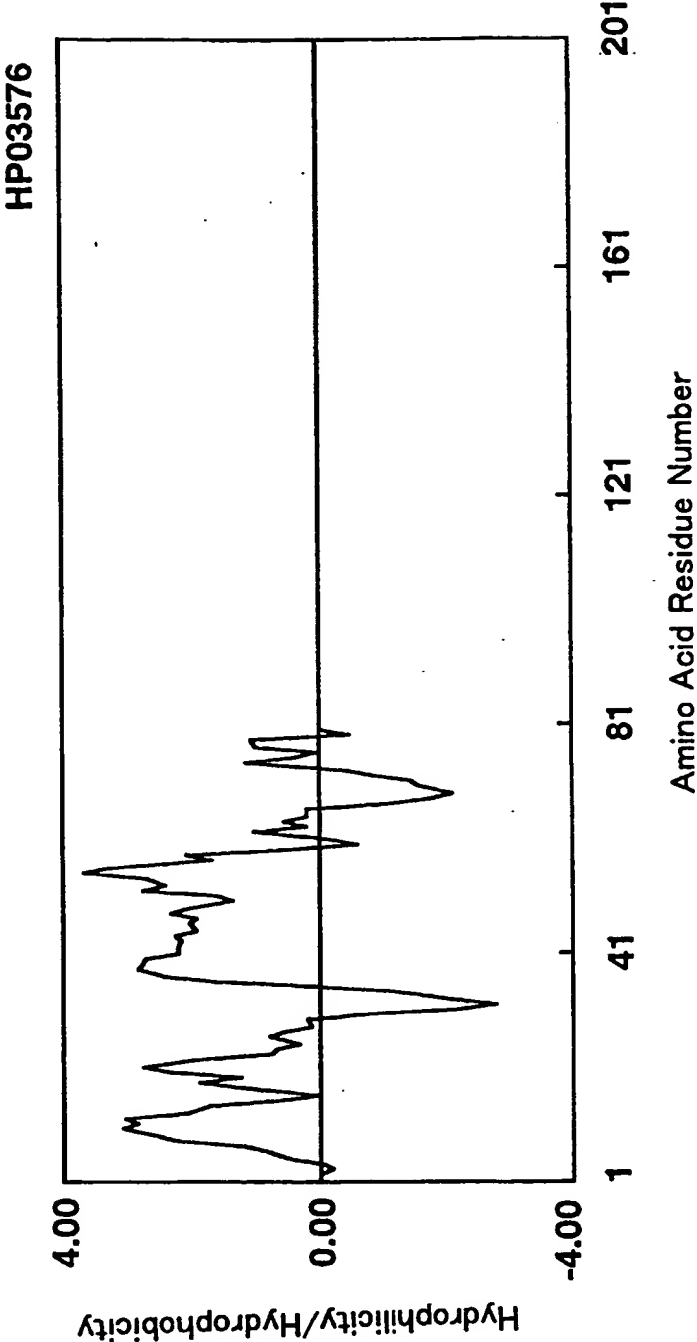


Fig.12

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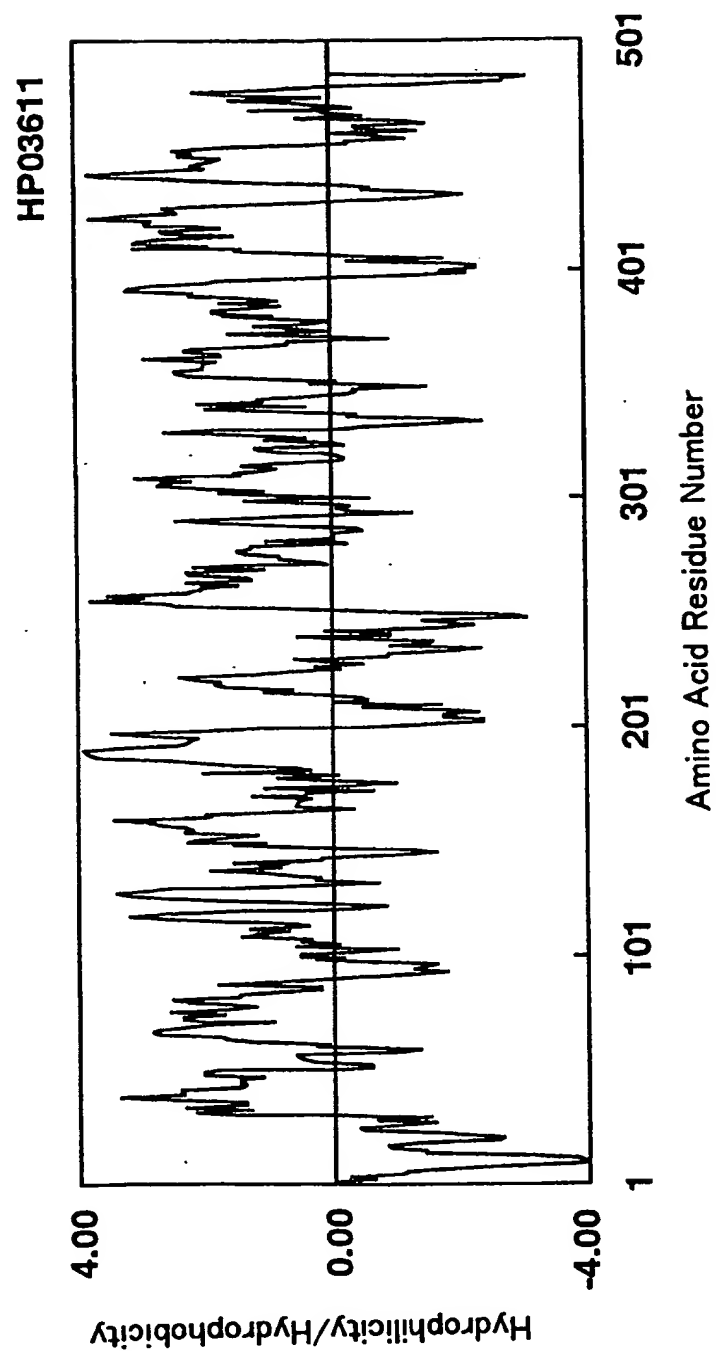


Fig.13

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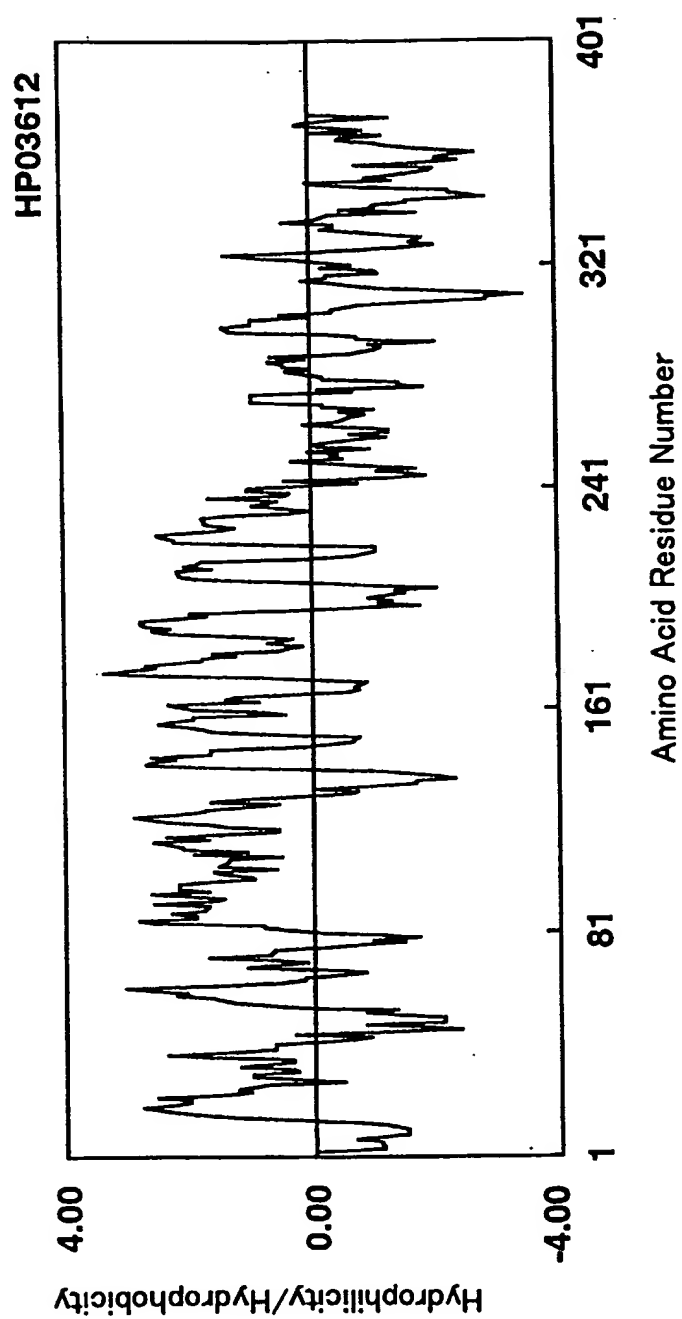


Fig.14

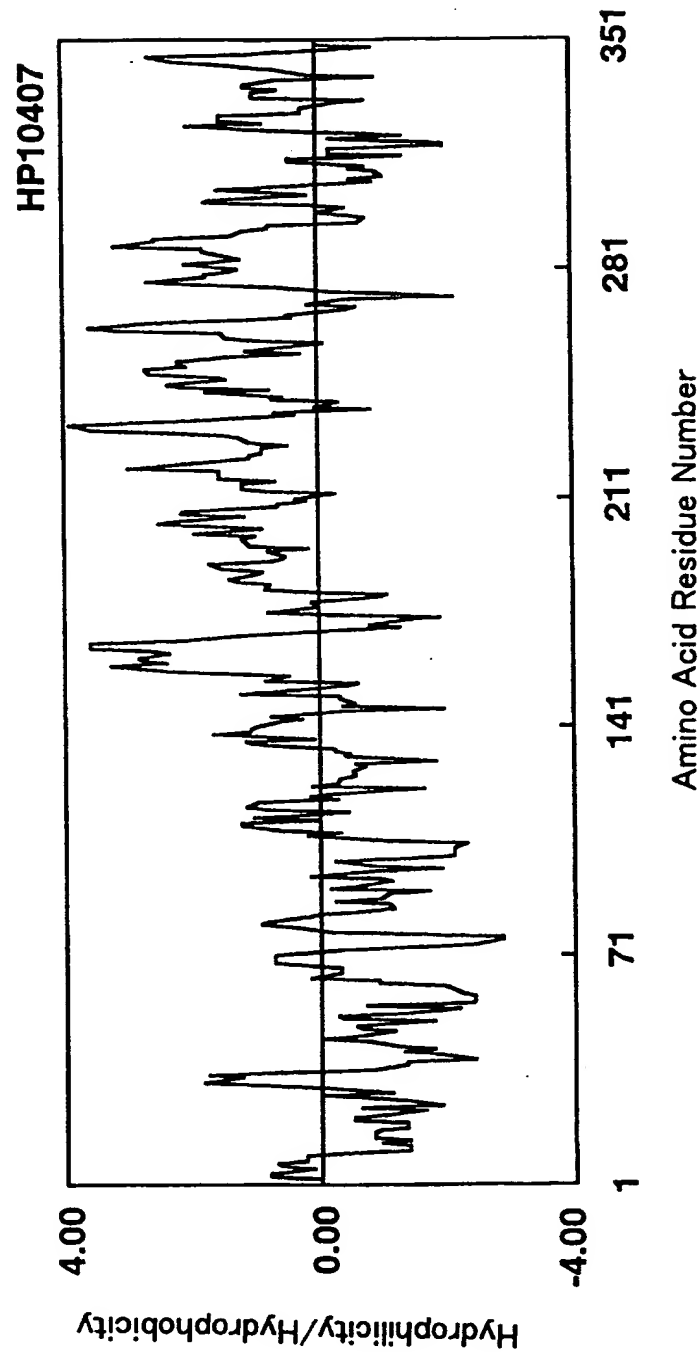


Fig.15

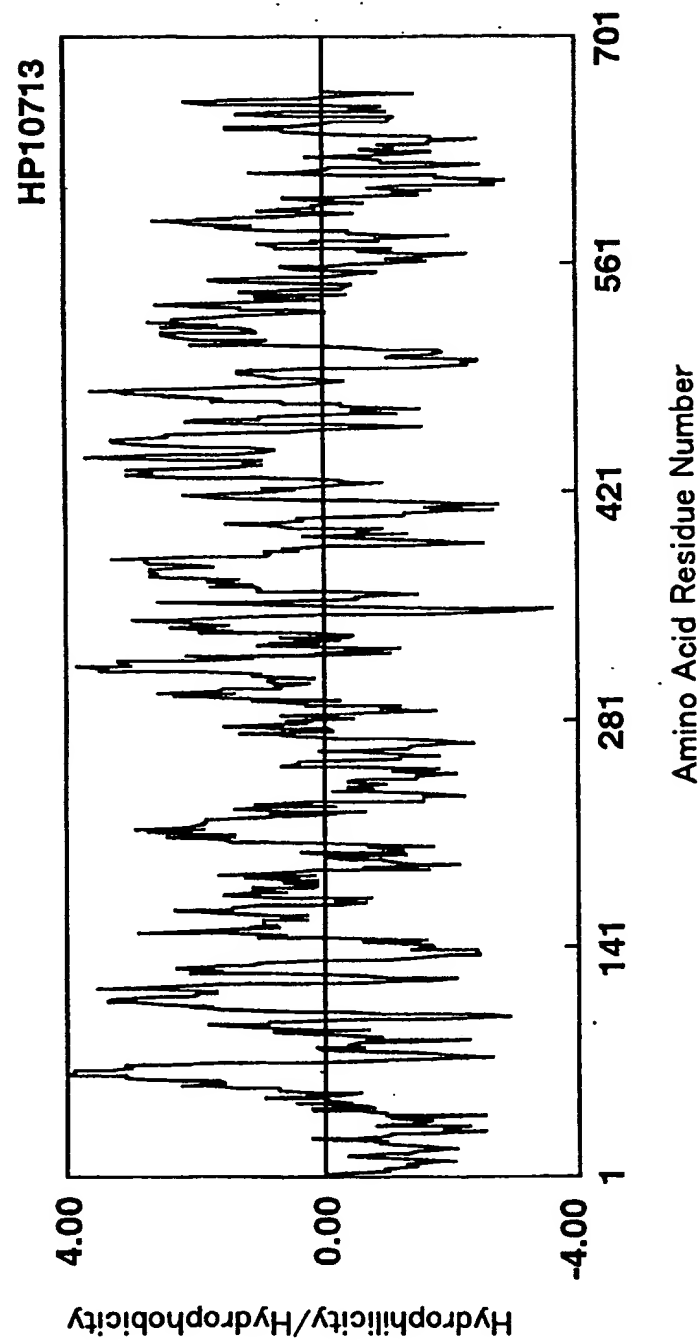


Fig.16

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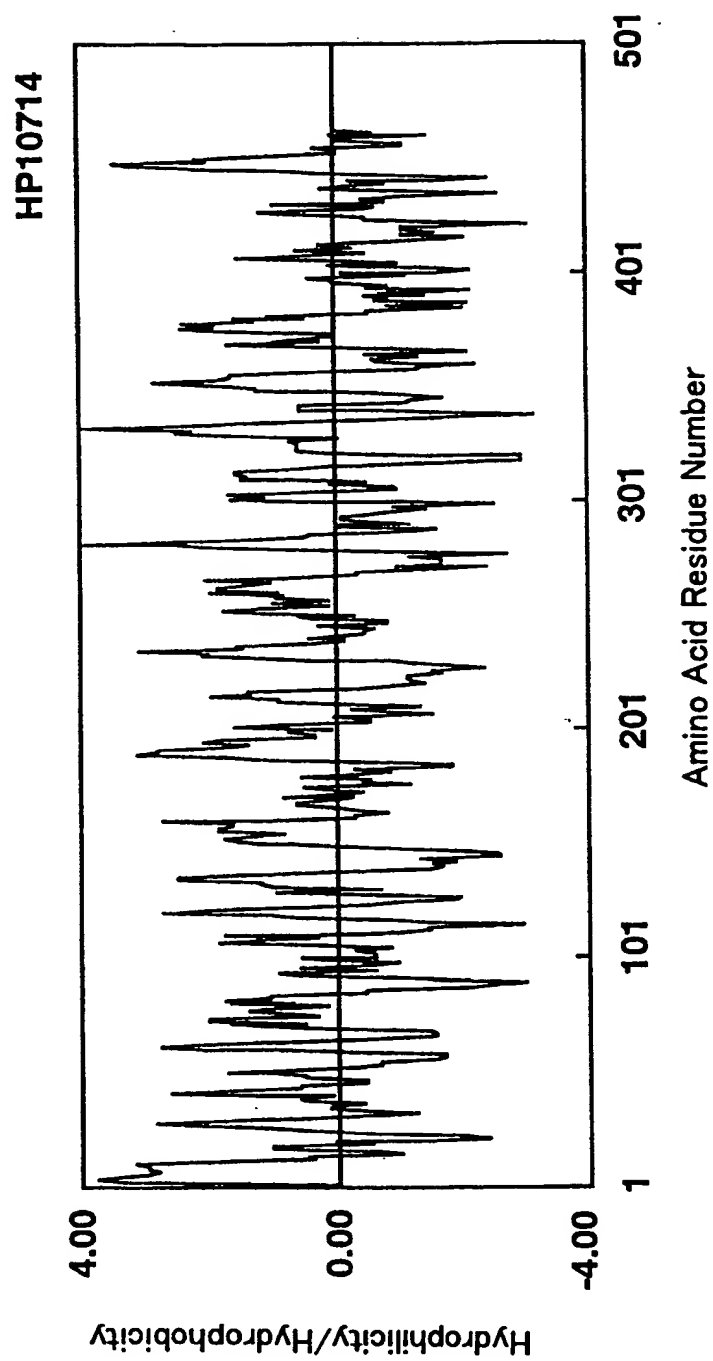


Fig.17

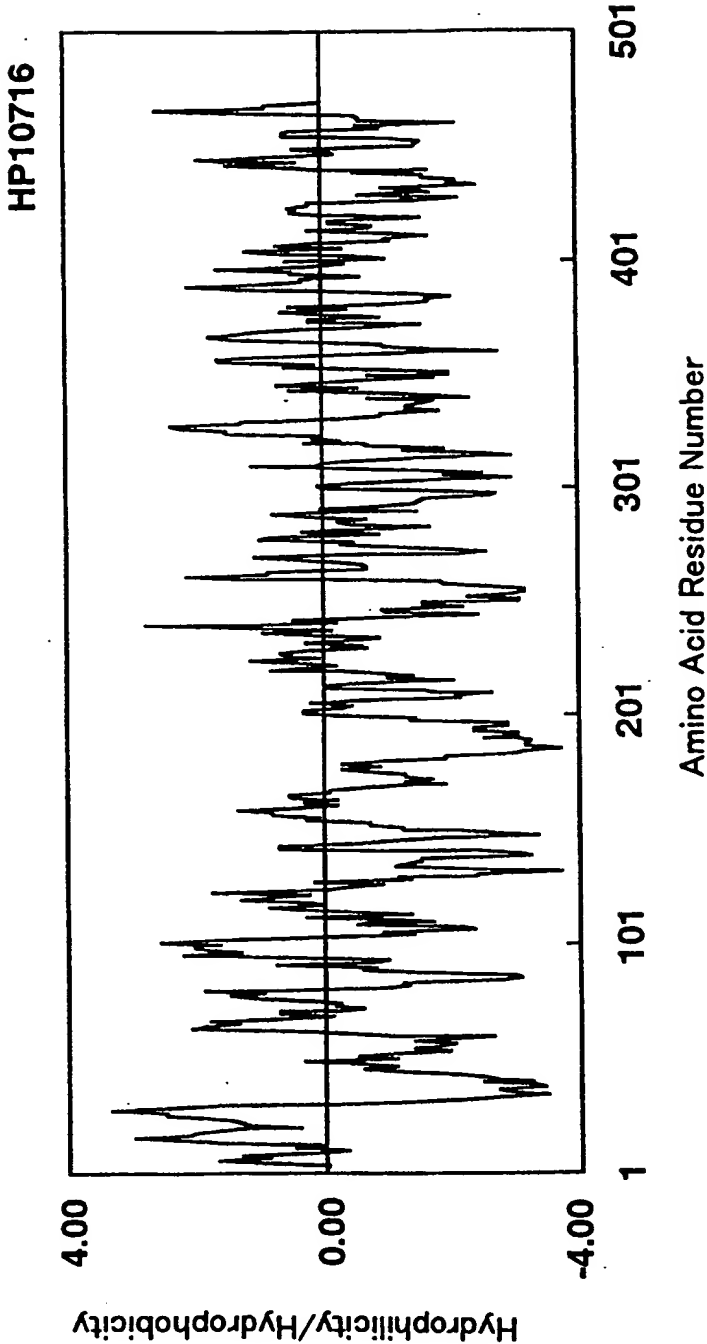


Fig.18

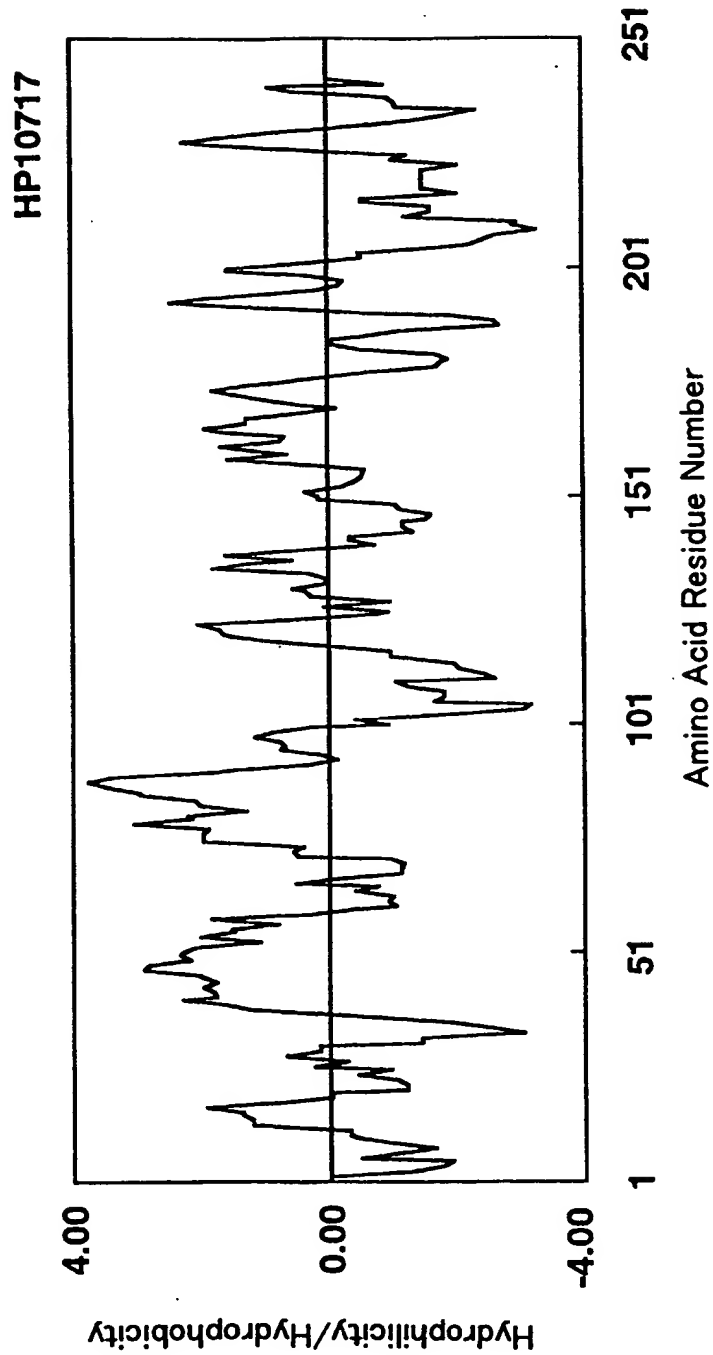


Fig.19

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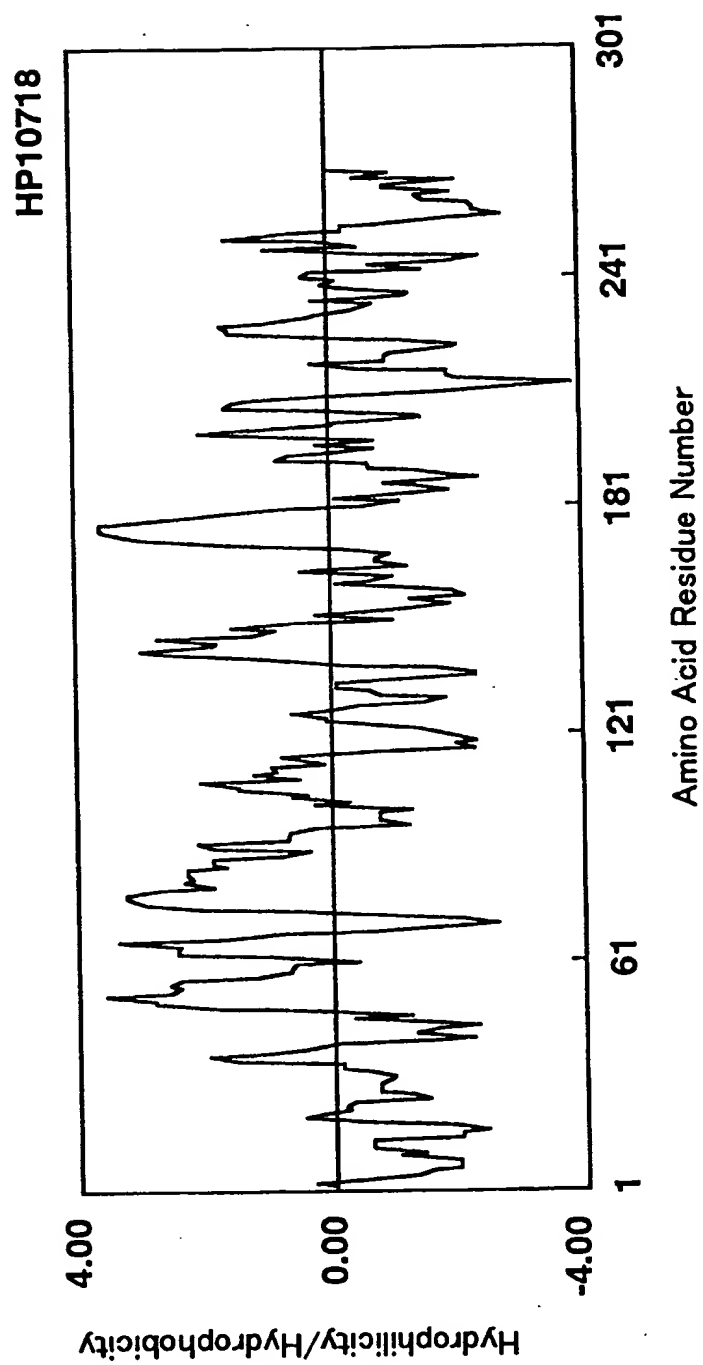


Fig.20

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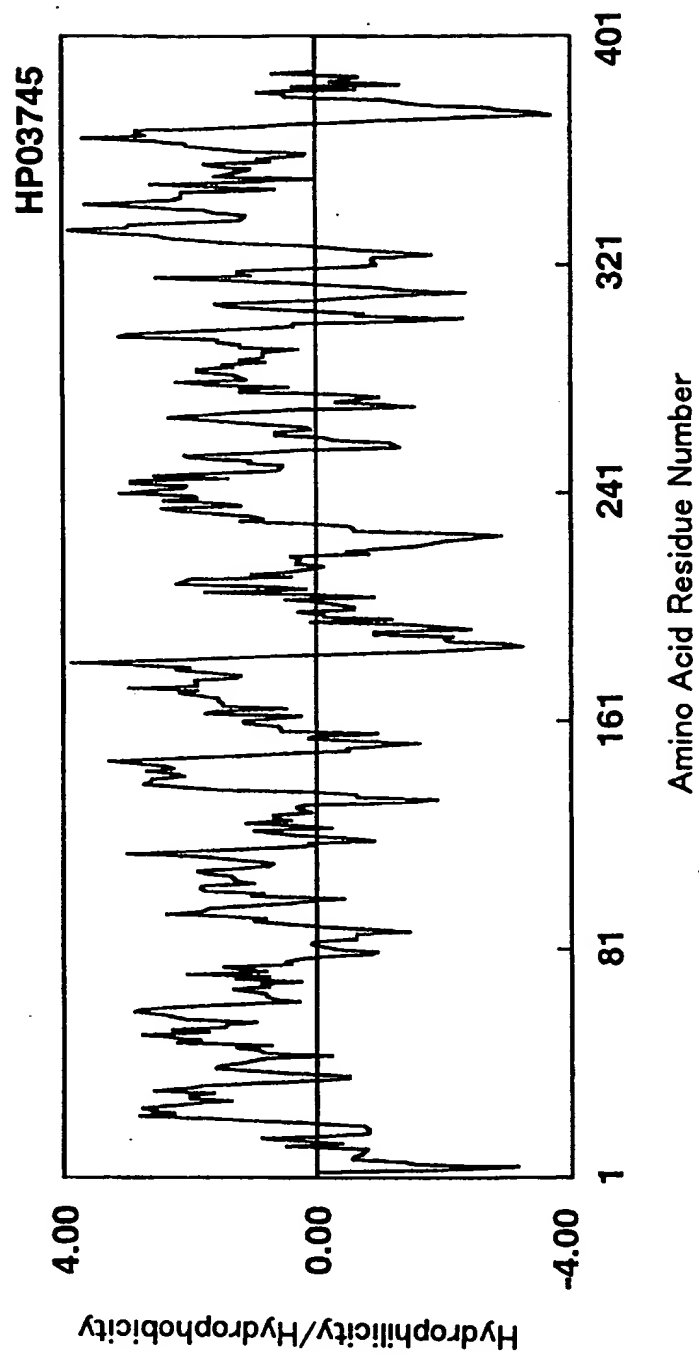


Fig.21

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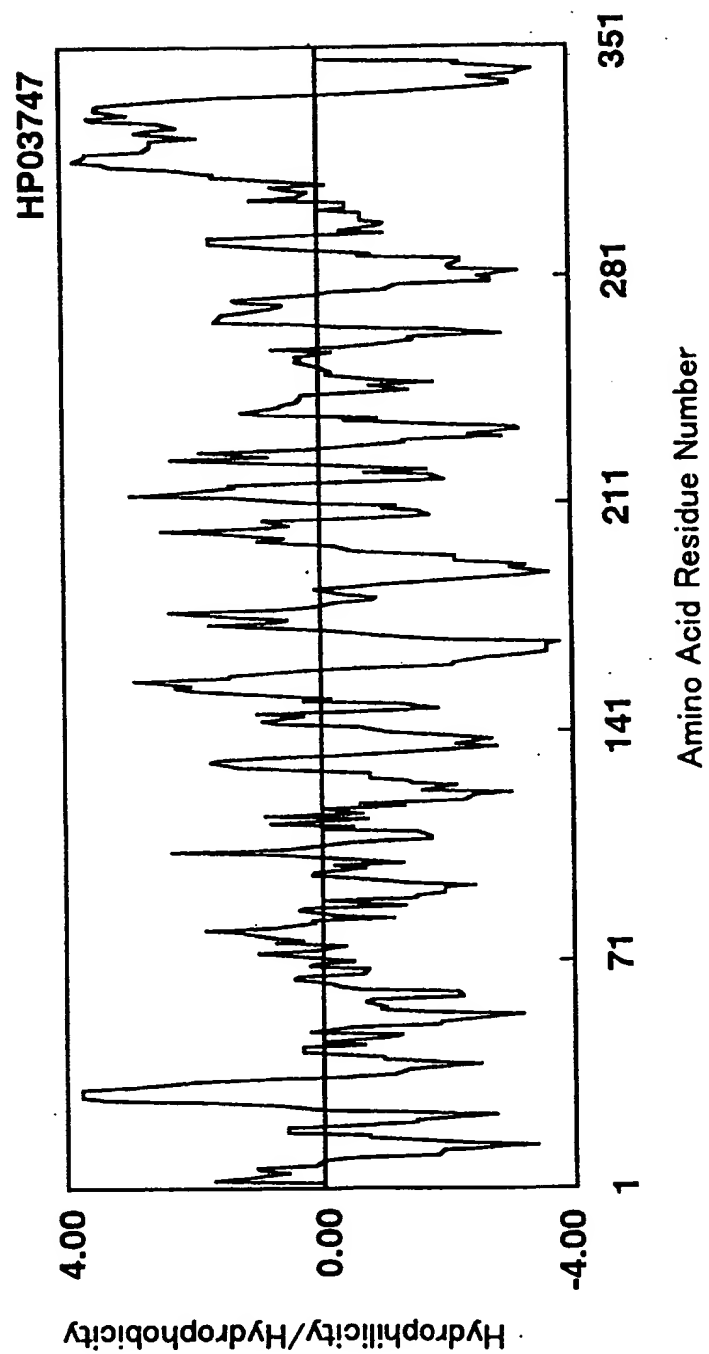


Fig.22

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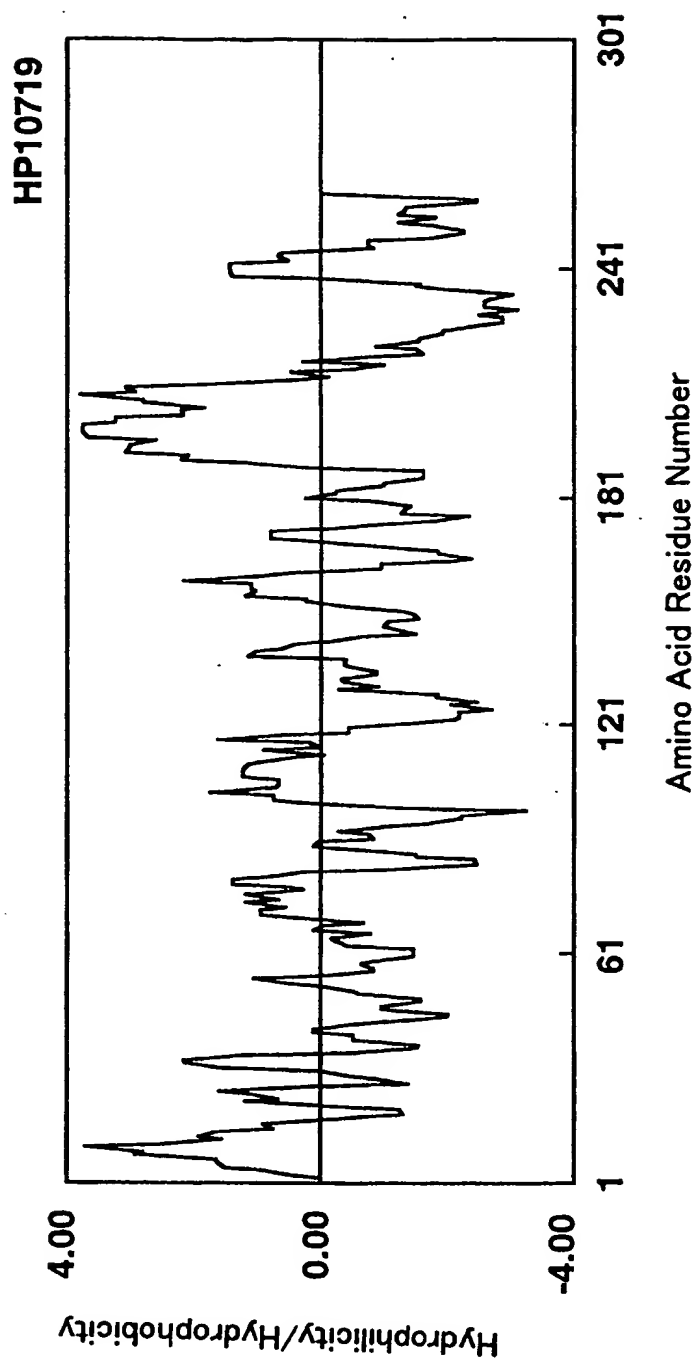


Fig.23

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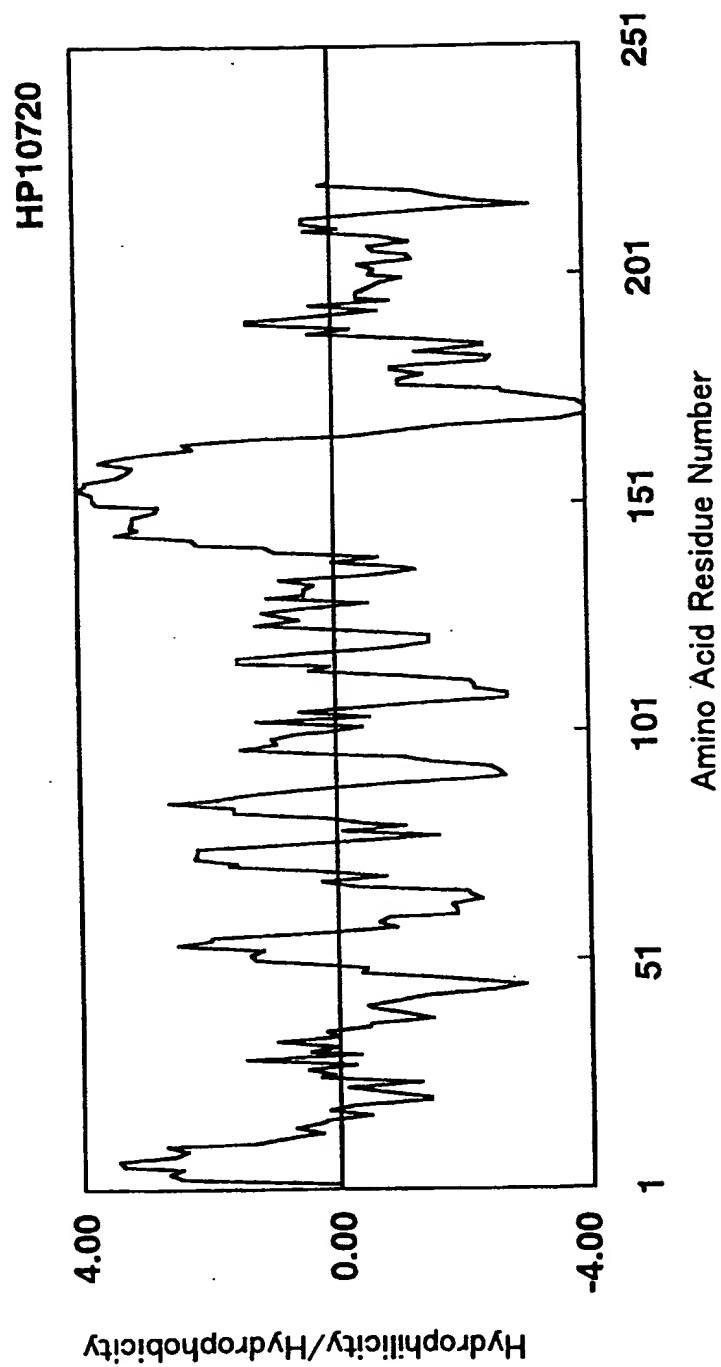


Fig.24

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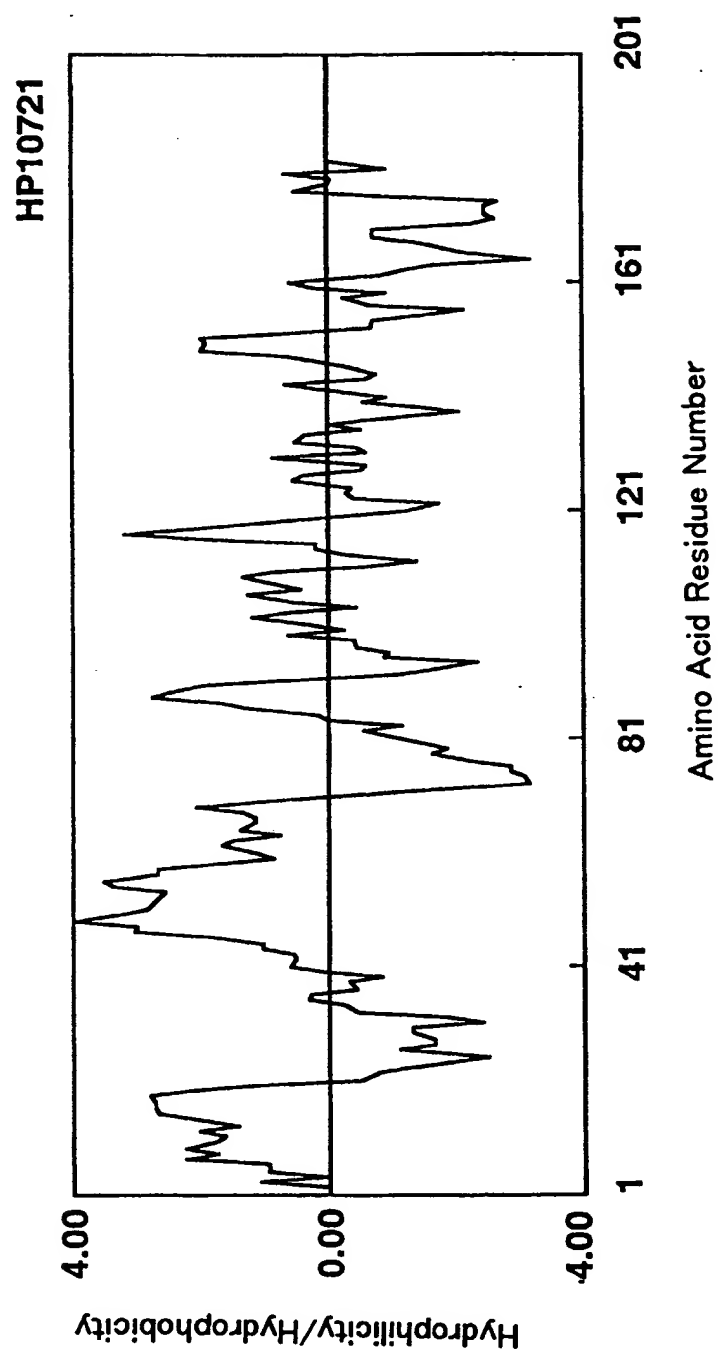


Fig.25

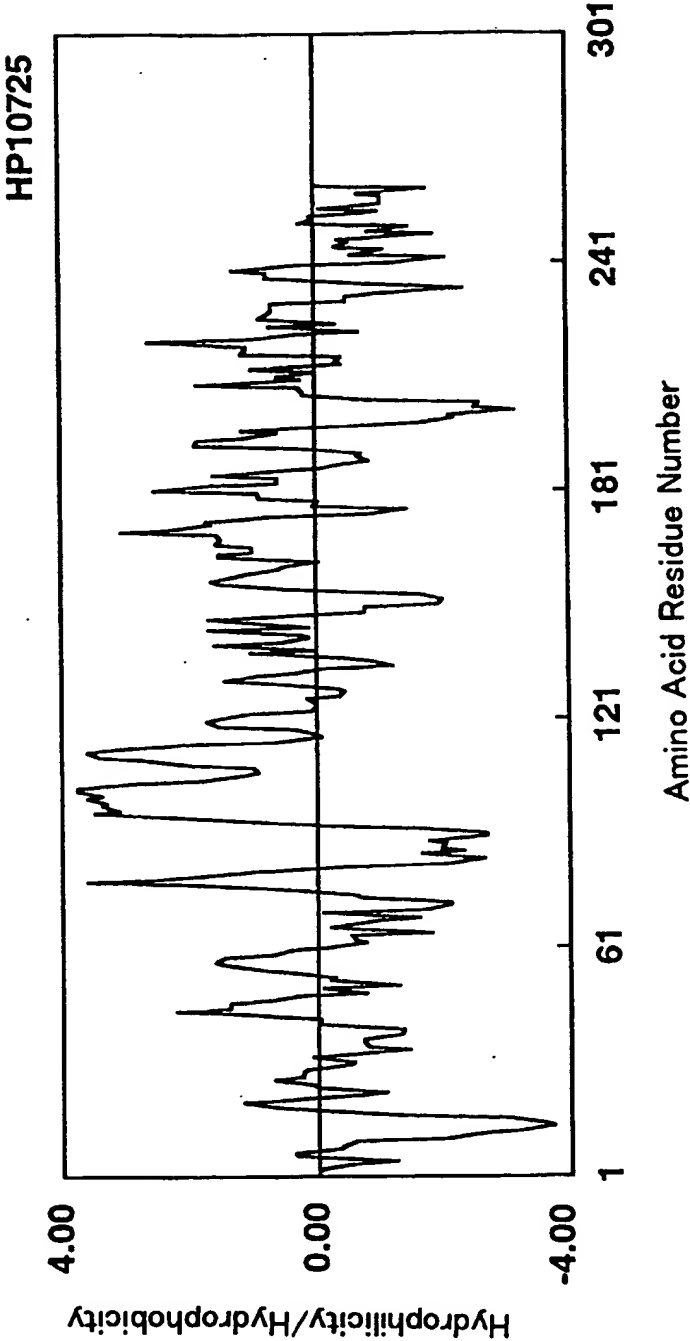


Fig.26

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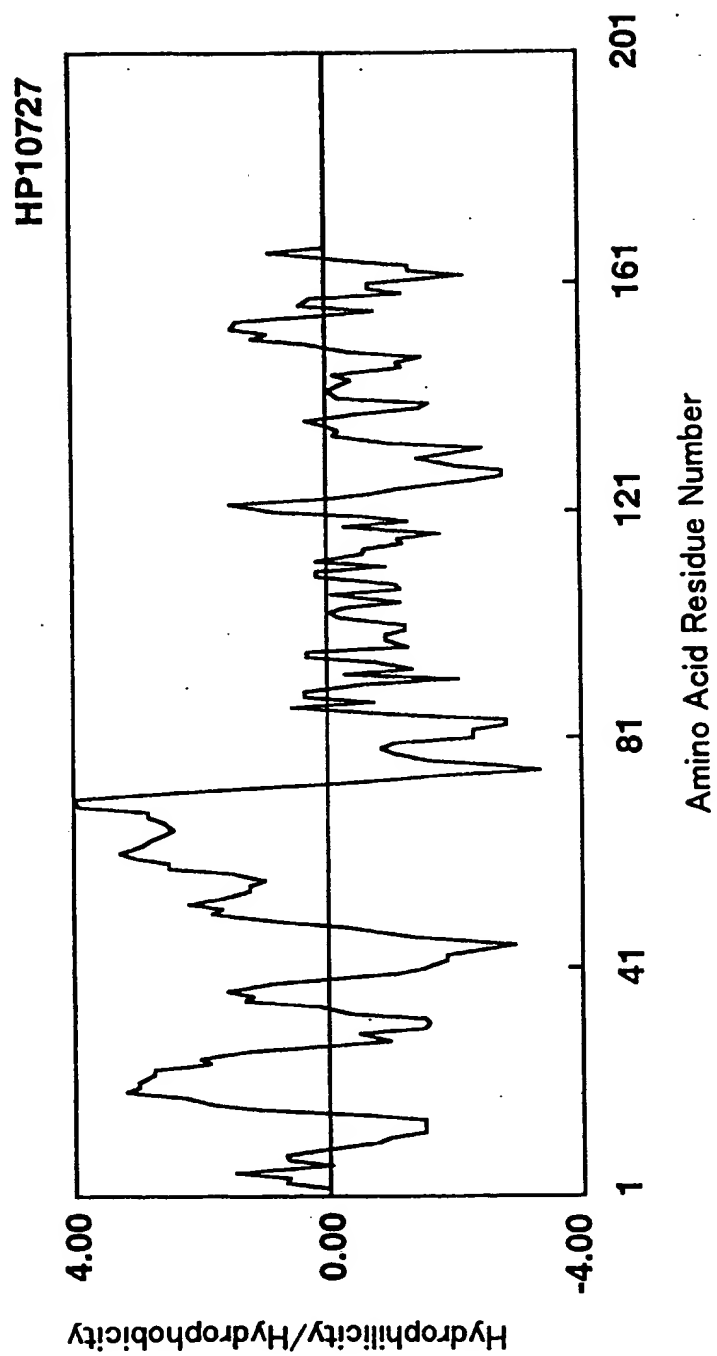


Fig.27

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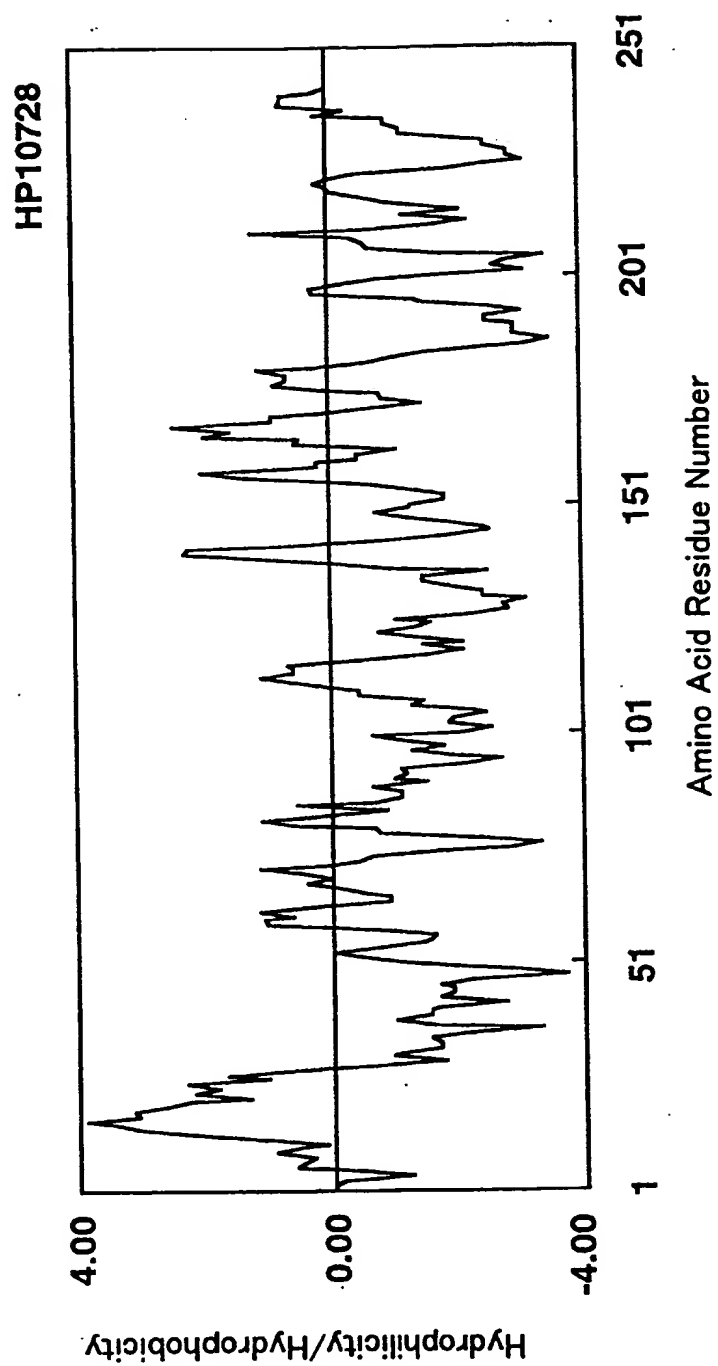


Fig.28

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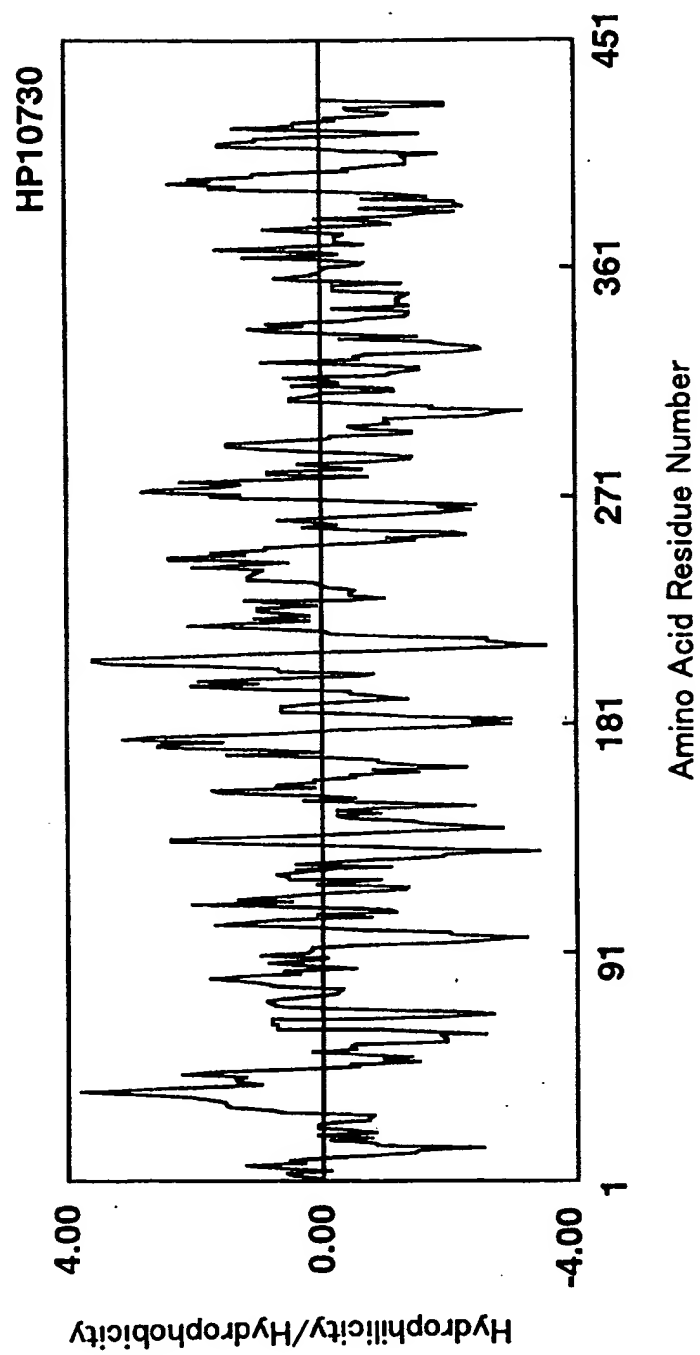


Fig.29

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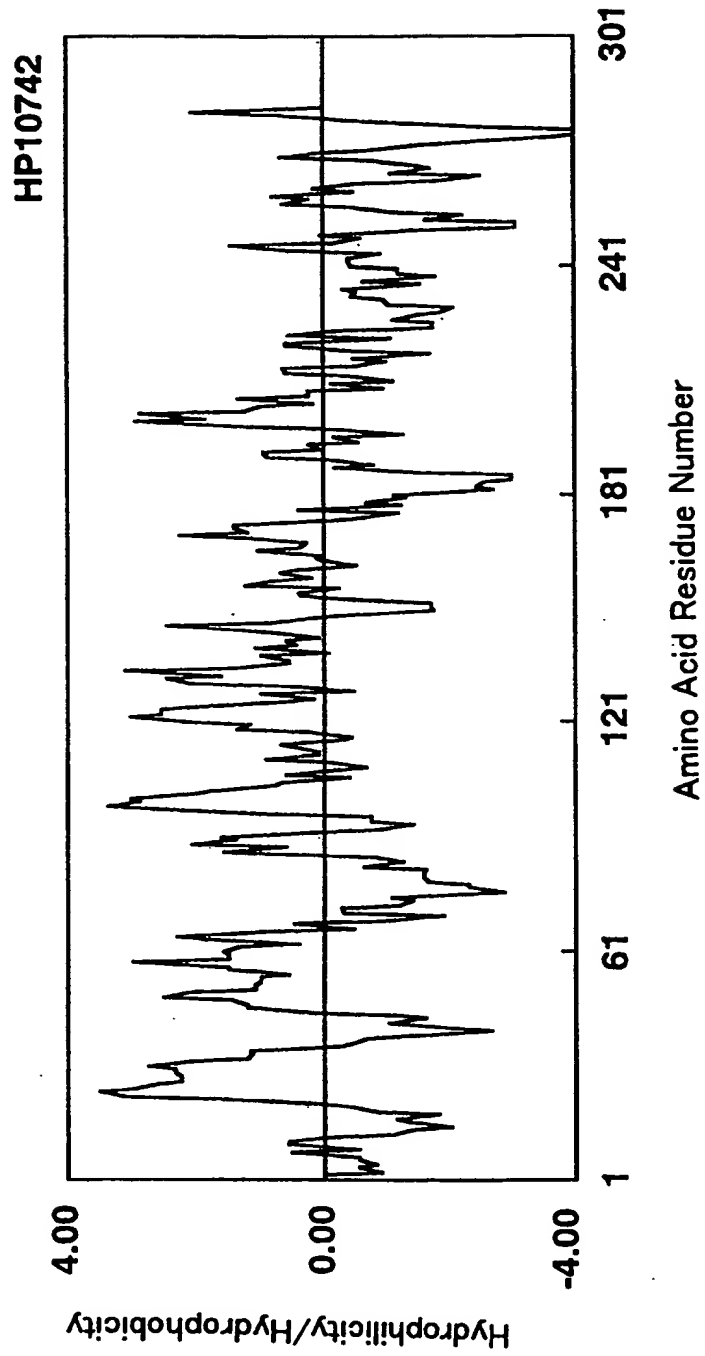


Fig.30

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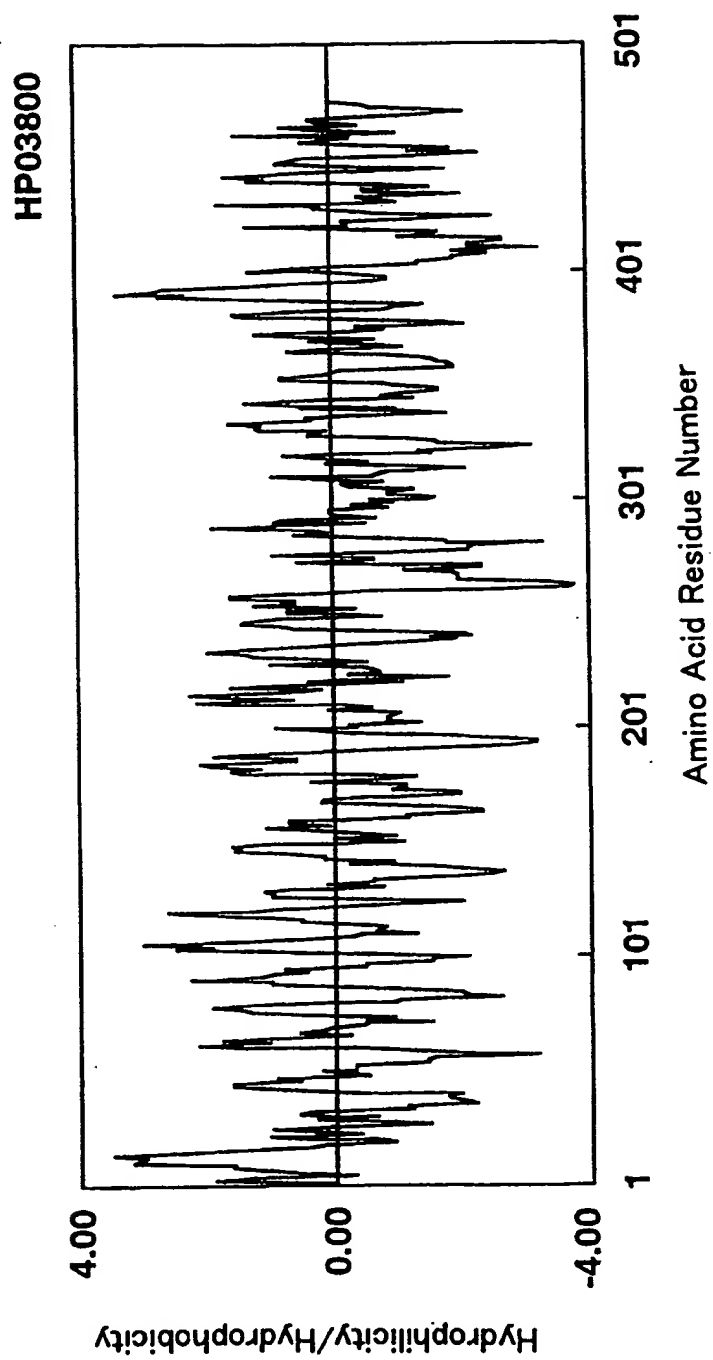


Fig.31

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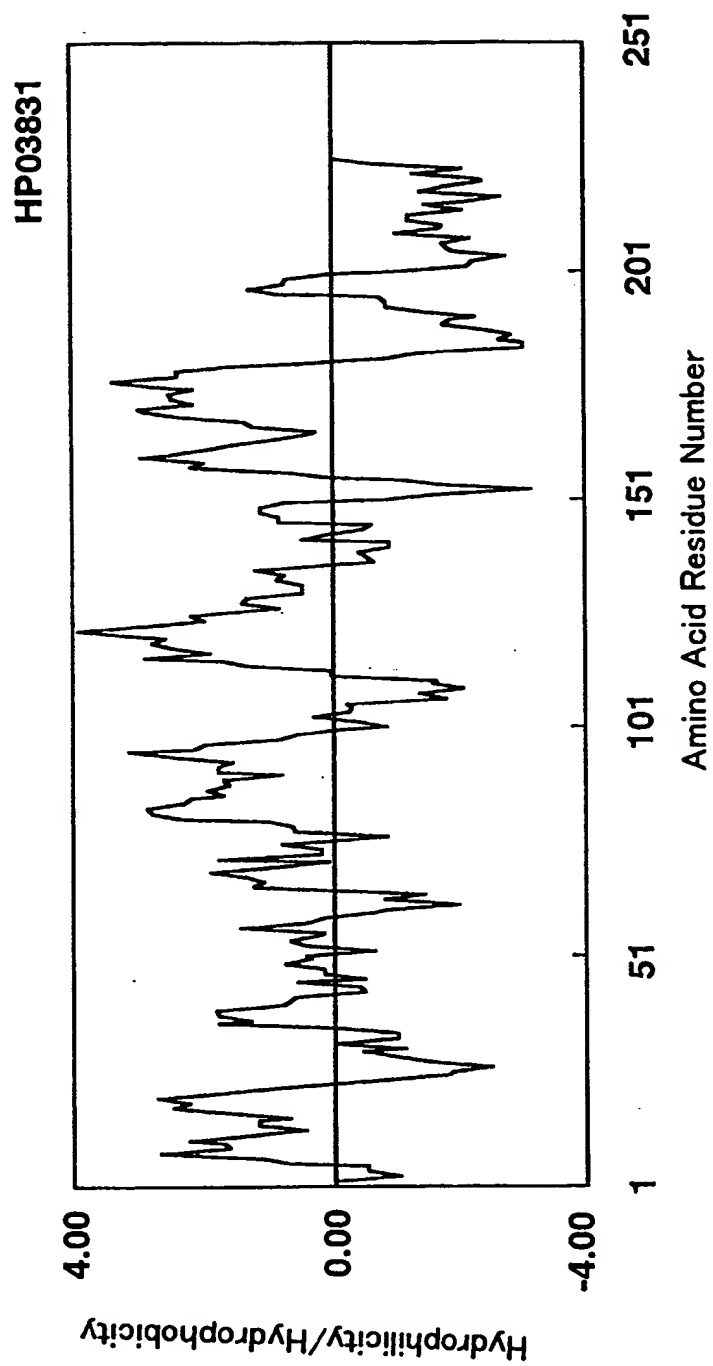


Fig.32

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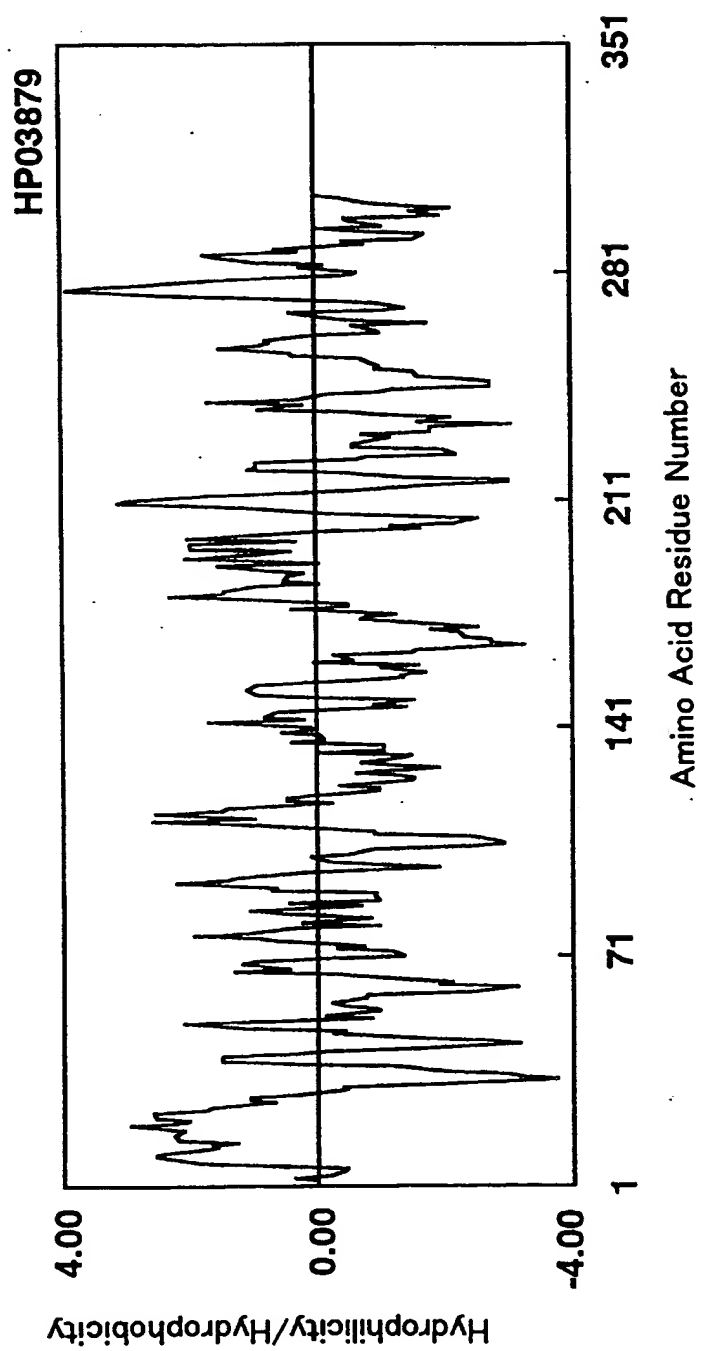


Fig.33

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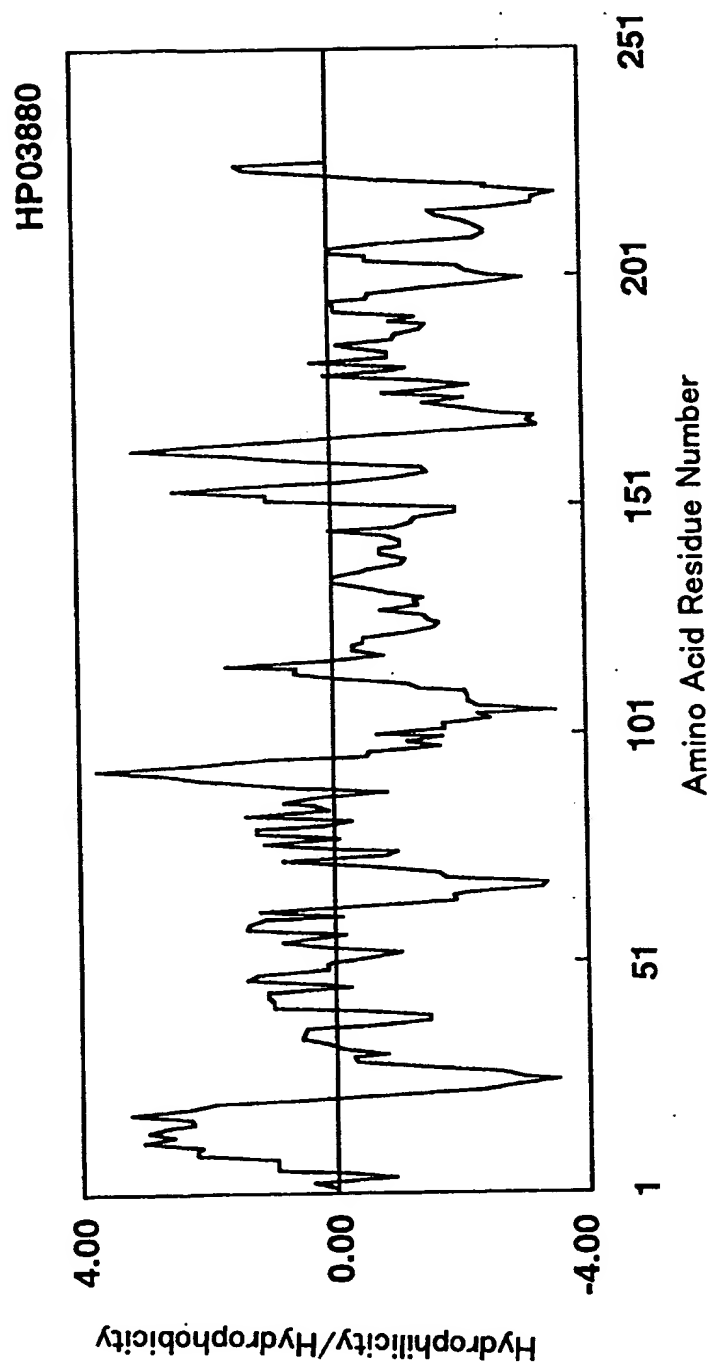


Fig.34

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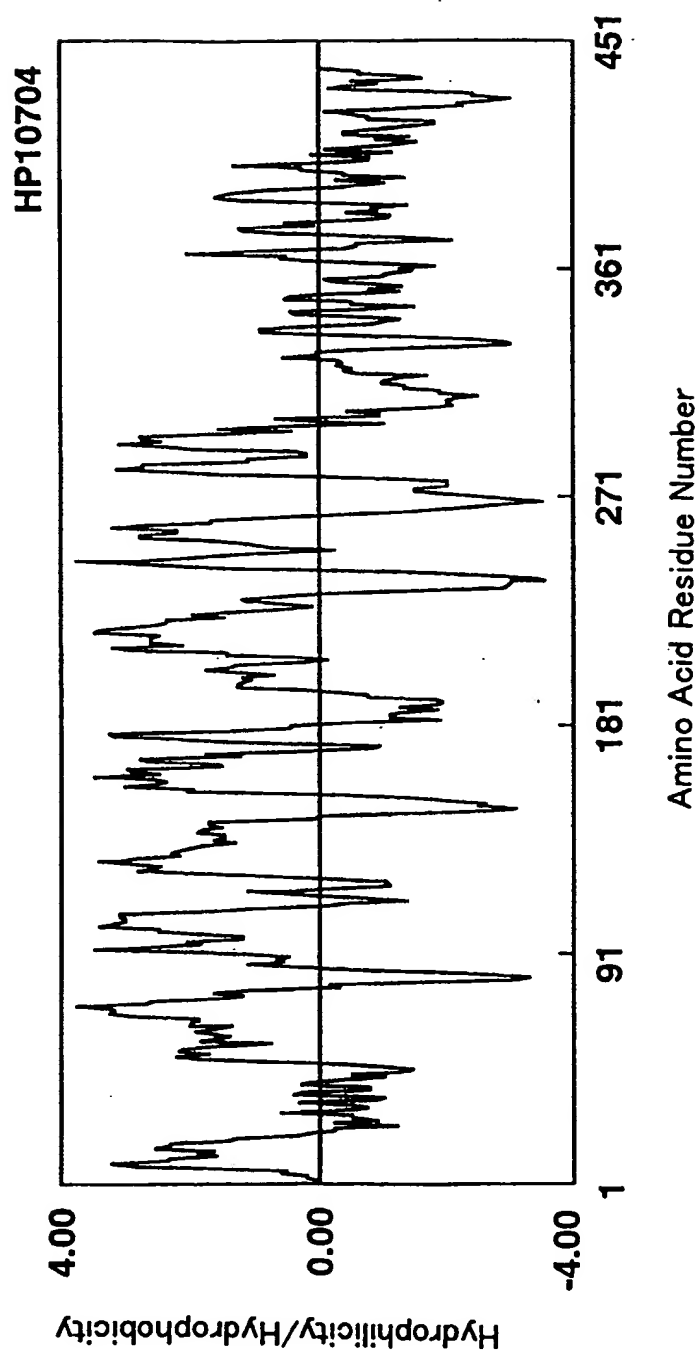


Fig.35

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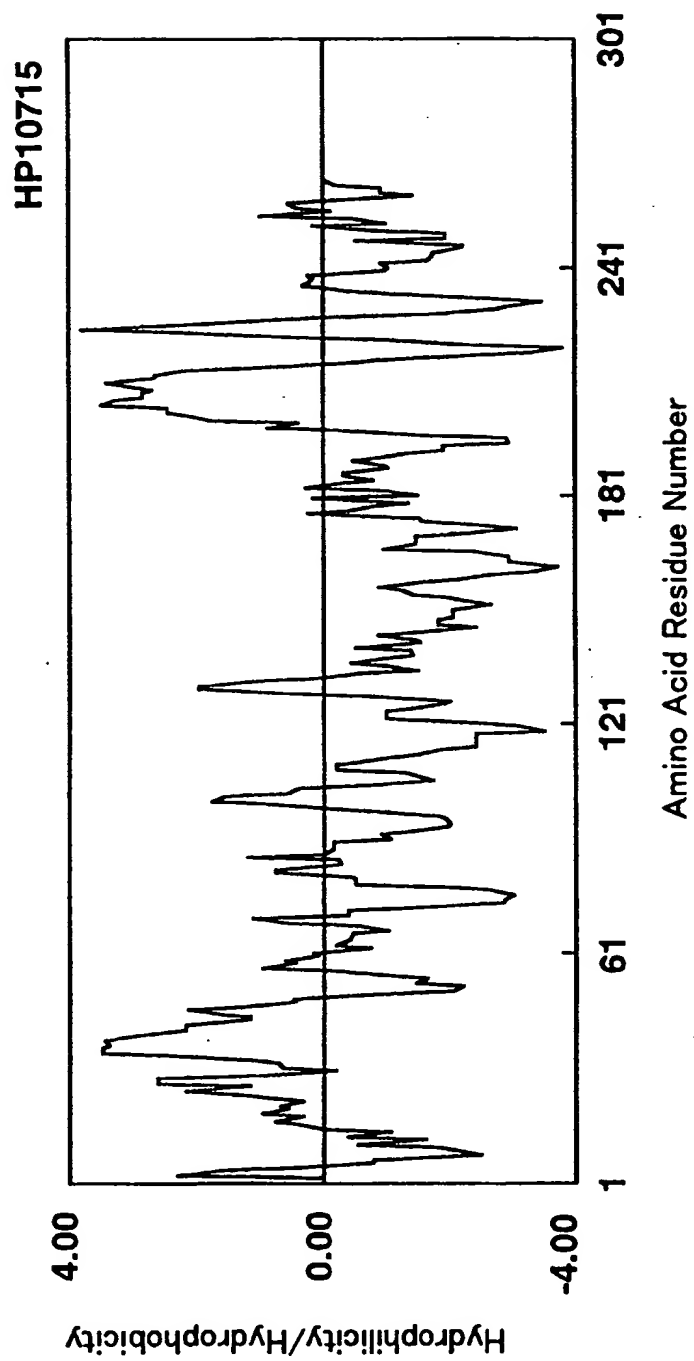


Fig.36

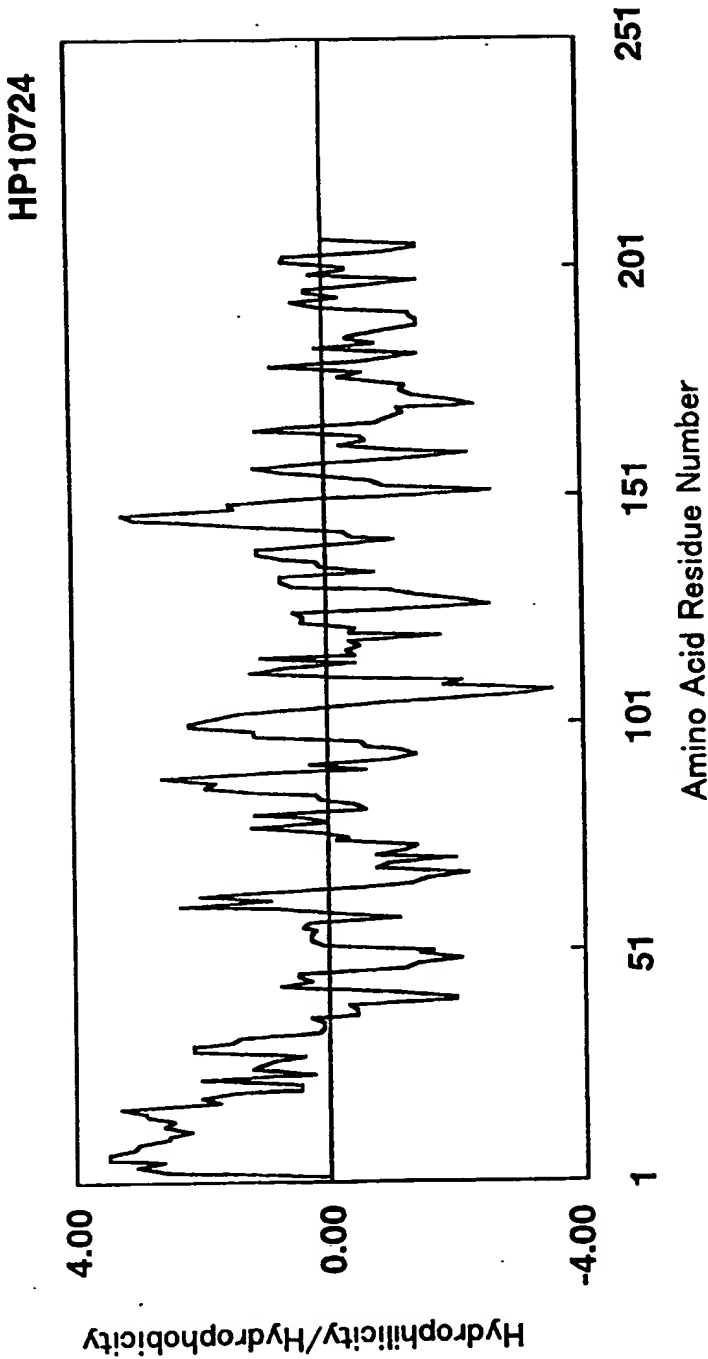


Fig.37

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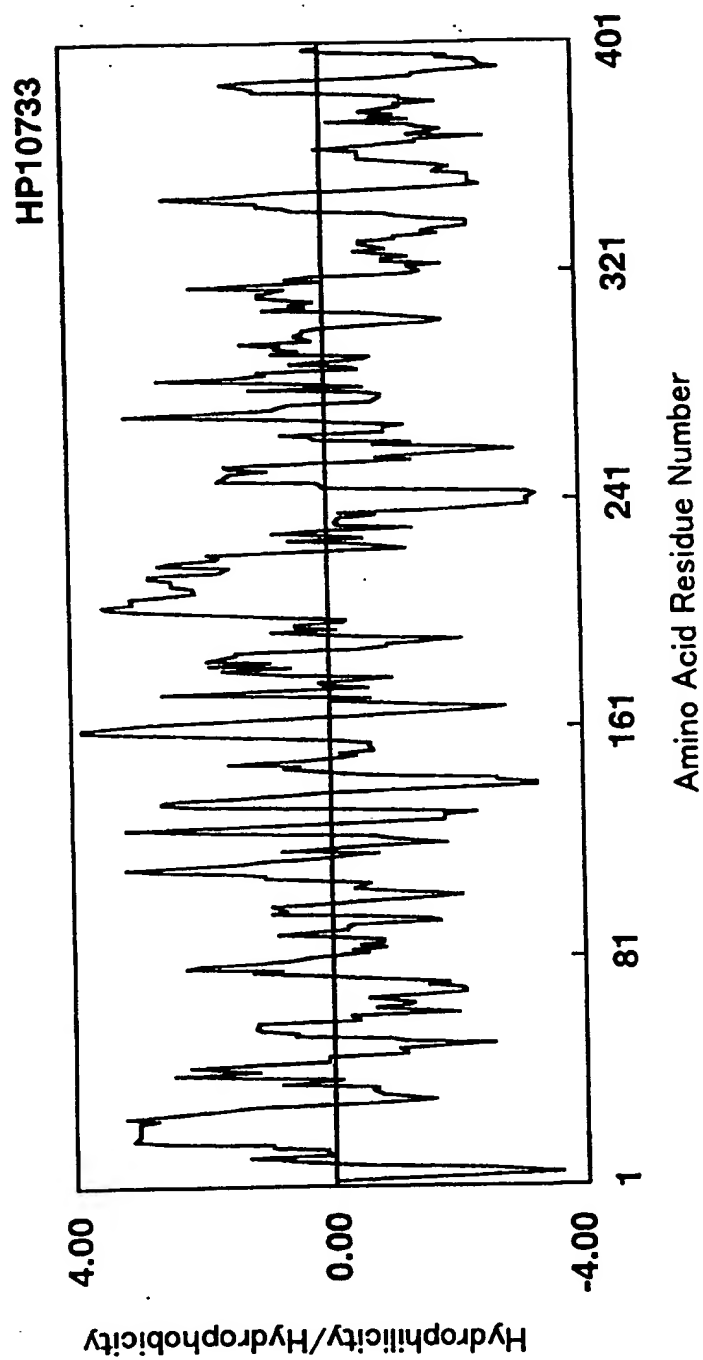


Fig.38

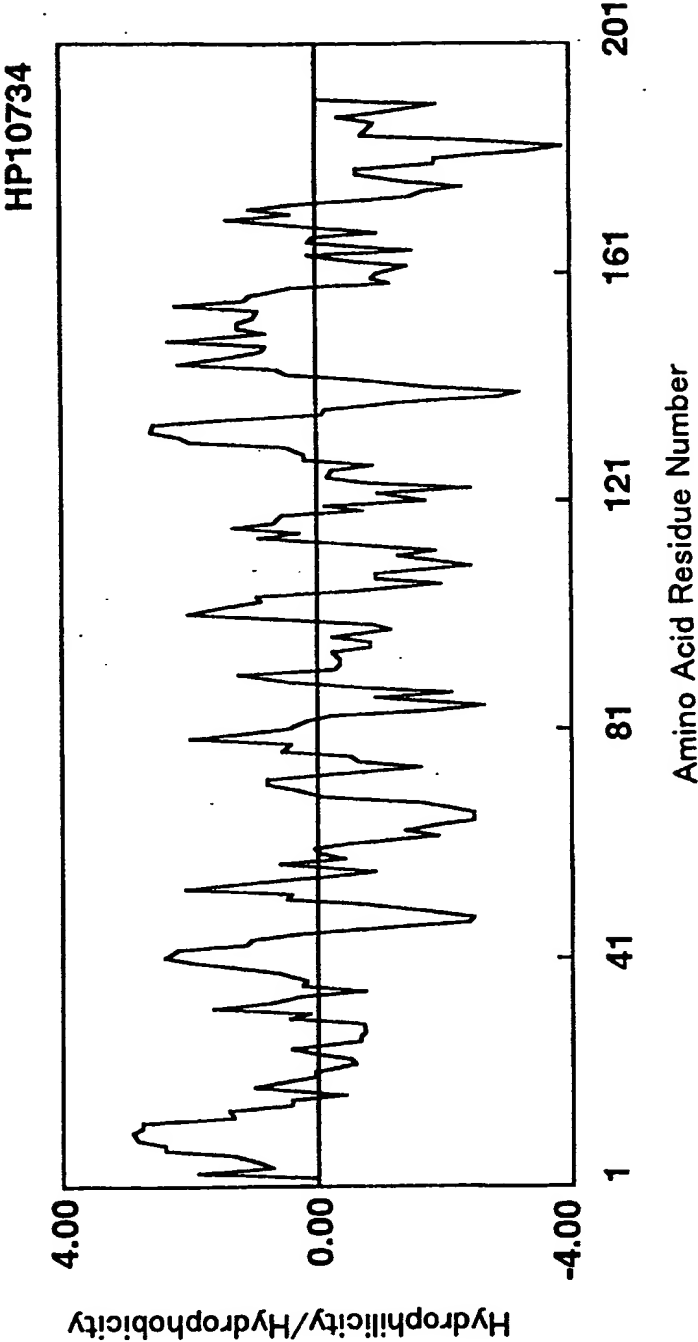


Fig.39

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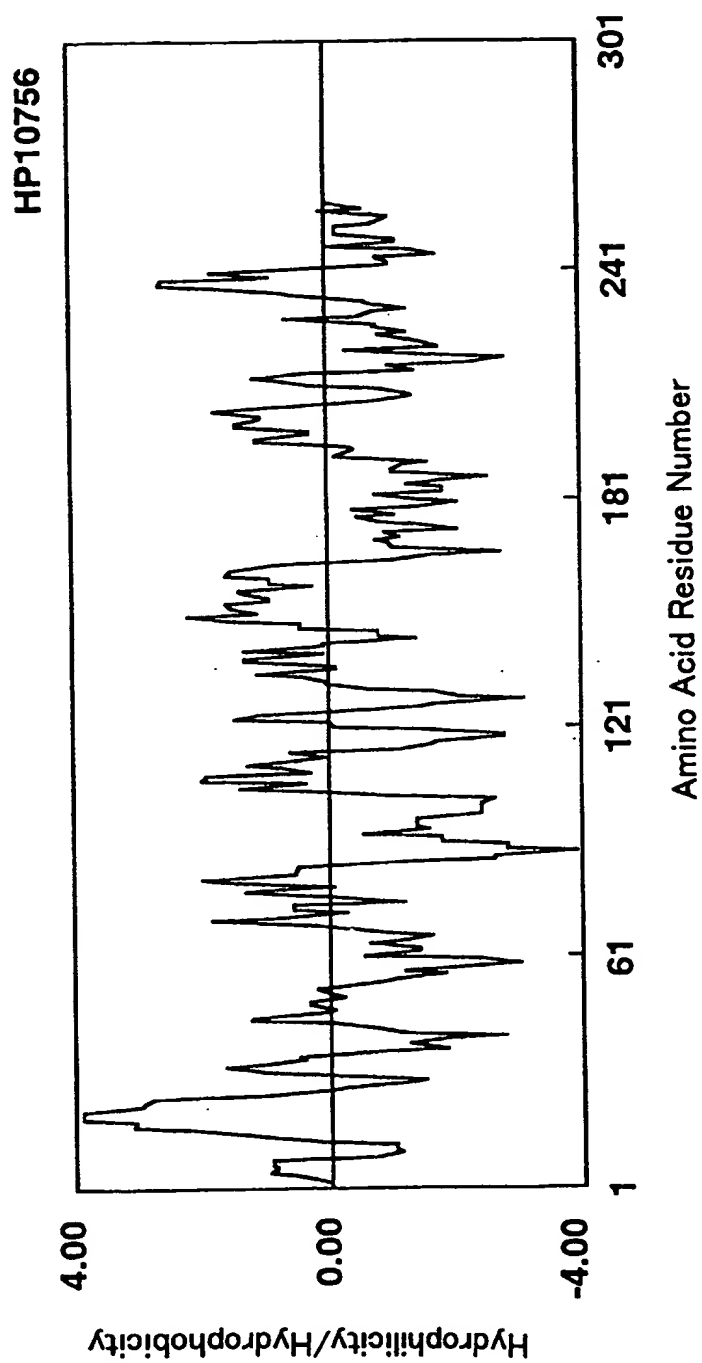


Fig.40

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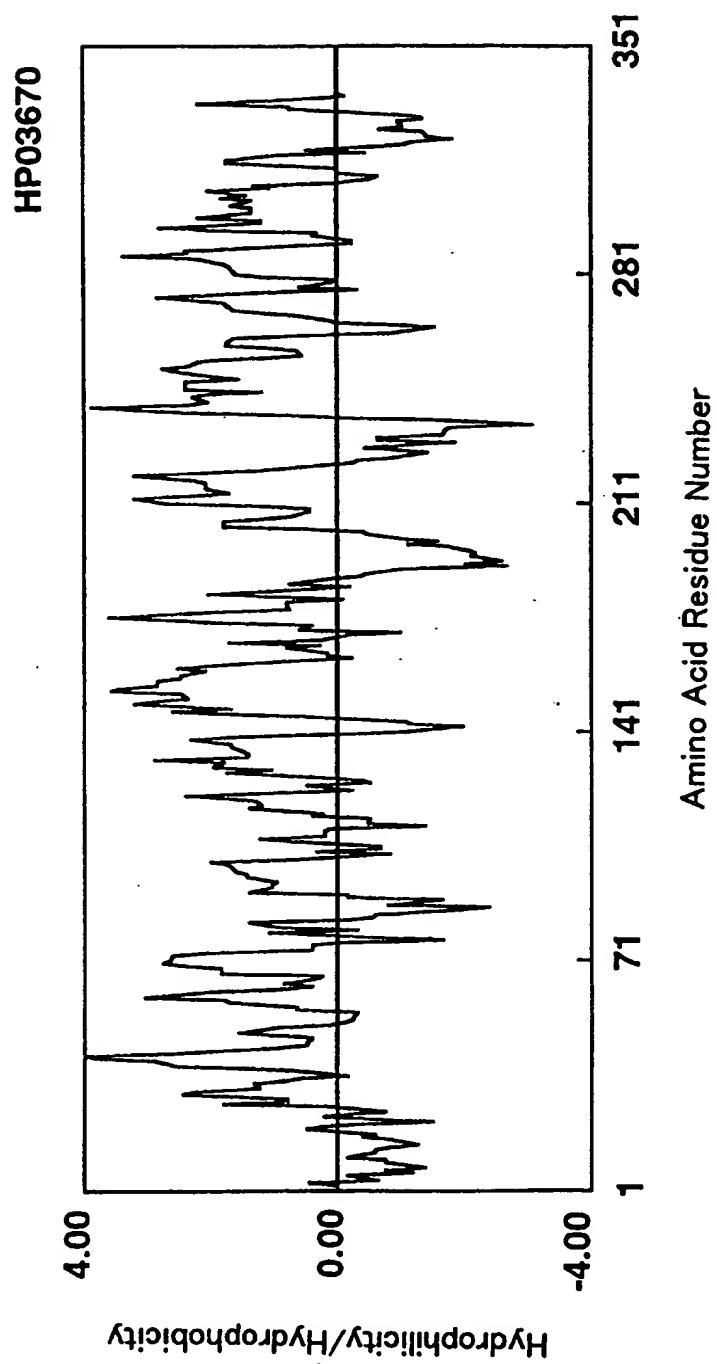


Fig.41

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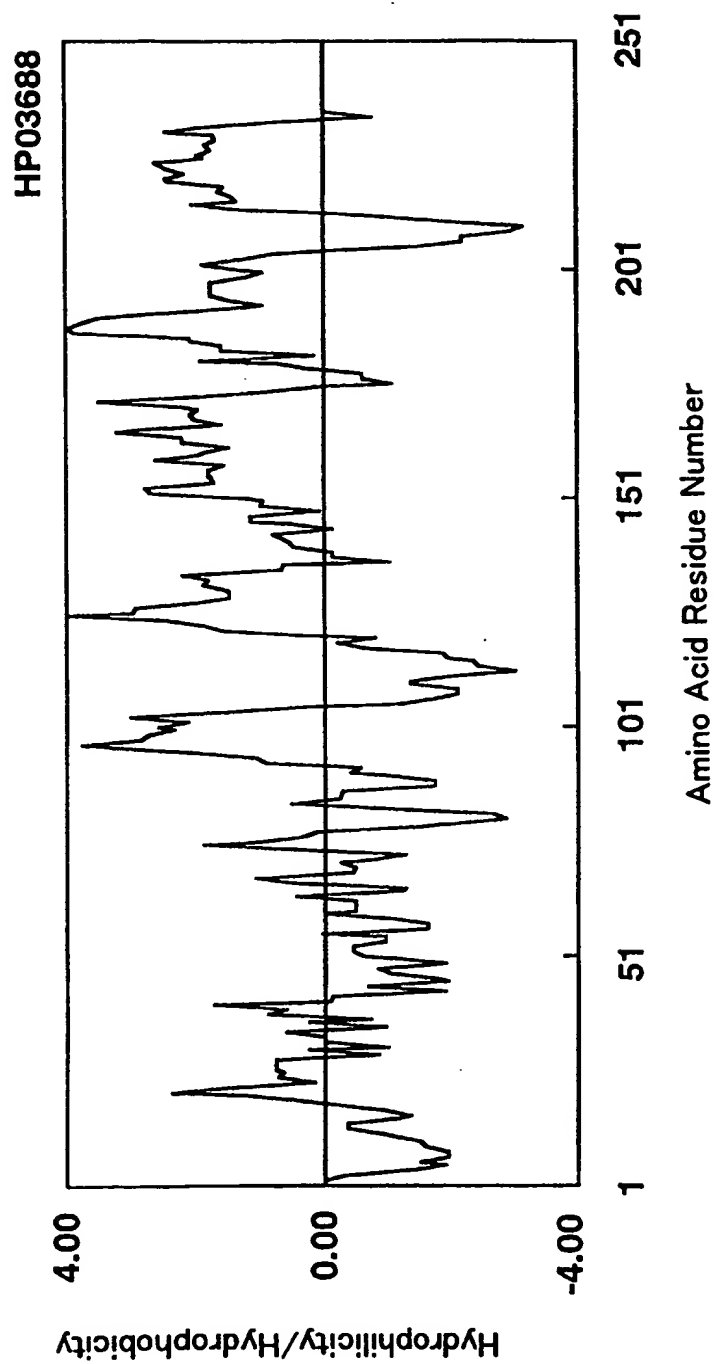


Fig.42

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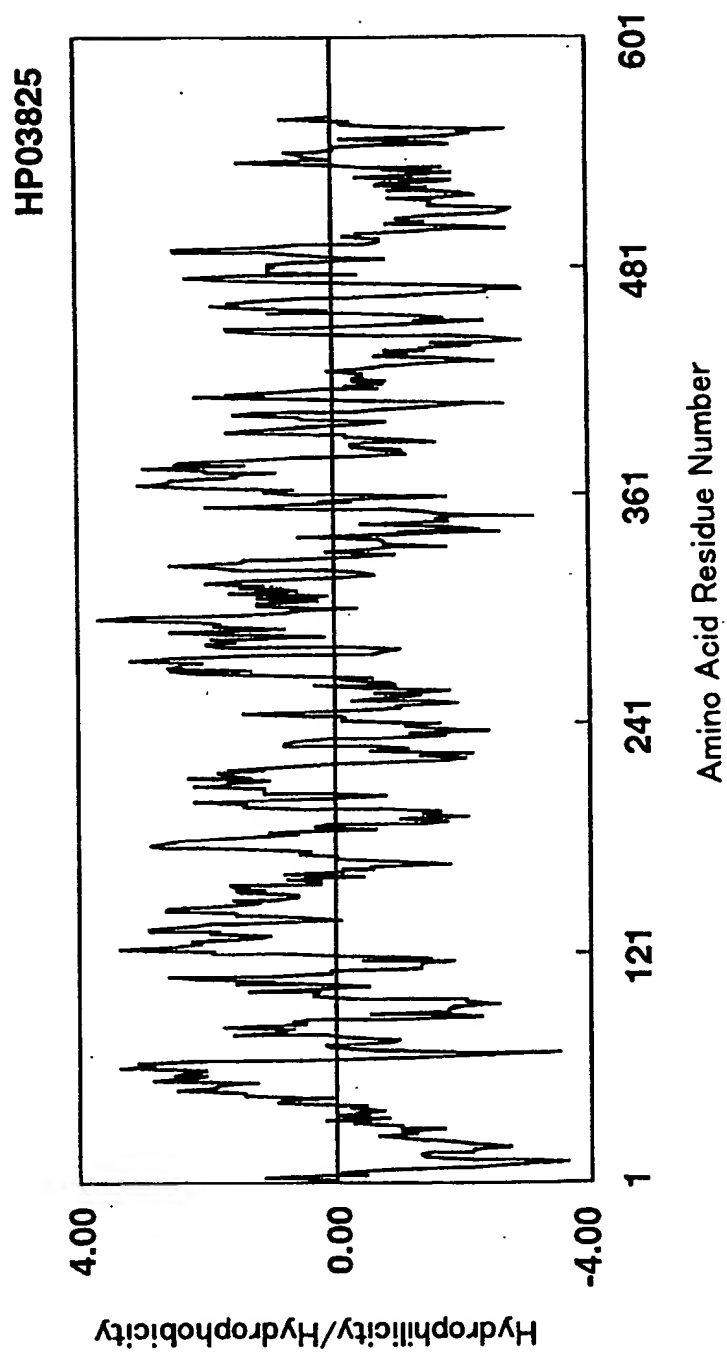


Fig.43

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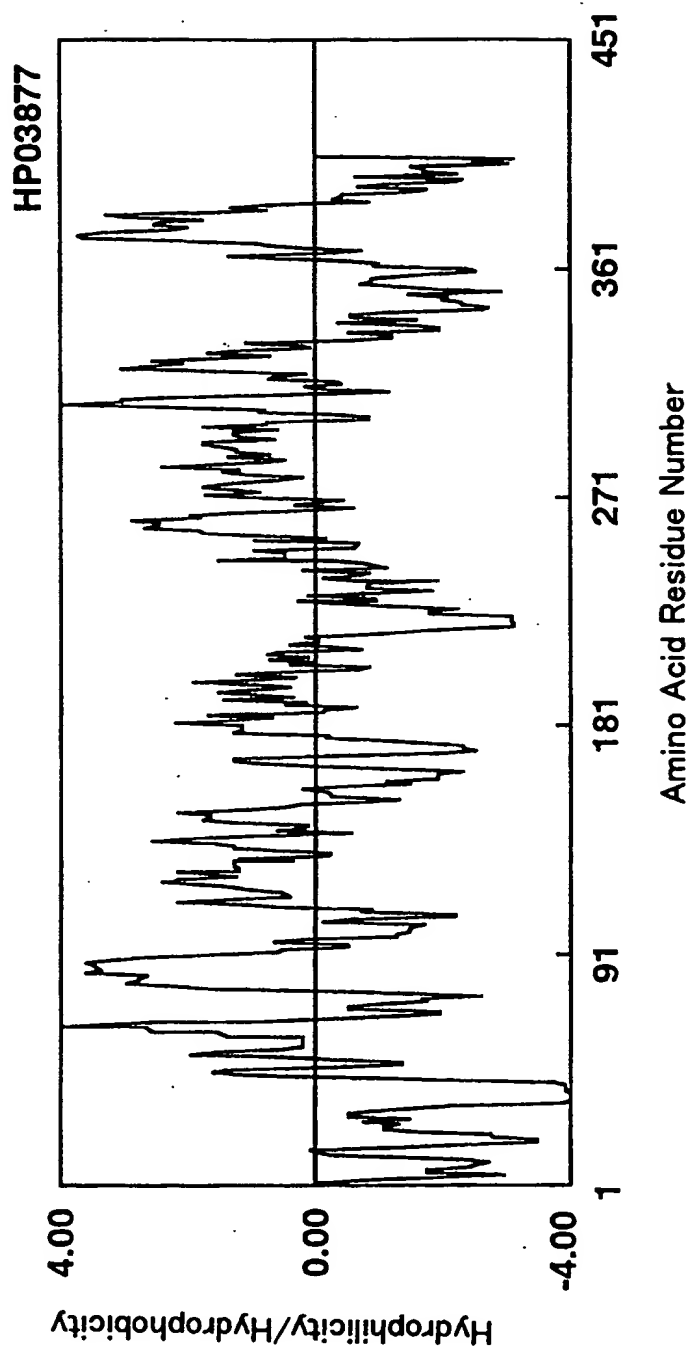


Fig.44

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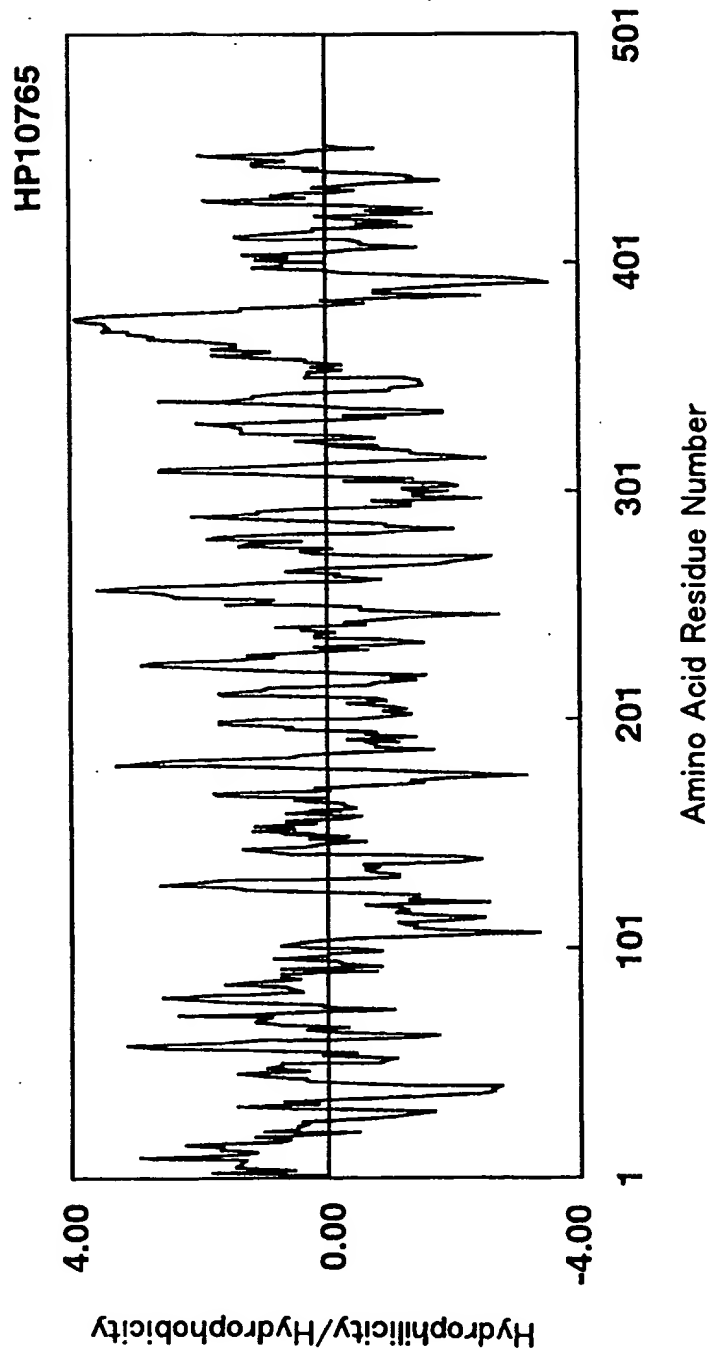


Fig.45

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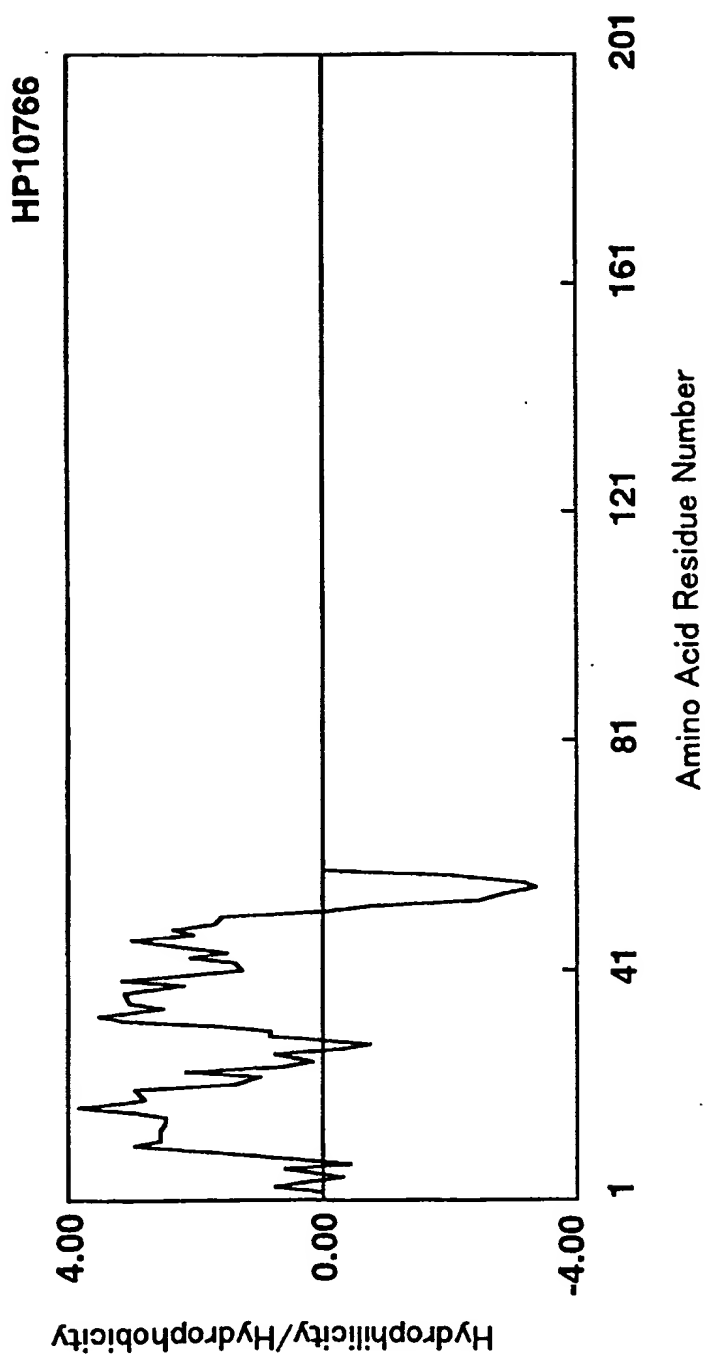


Fig.46

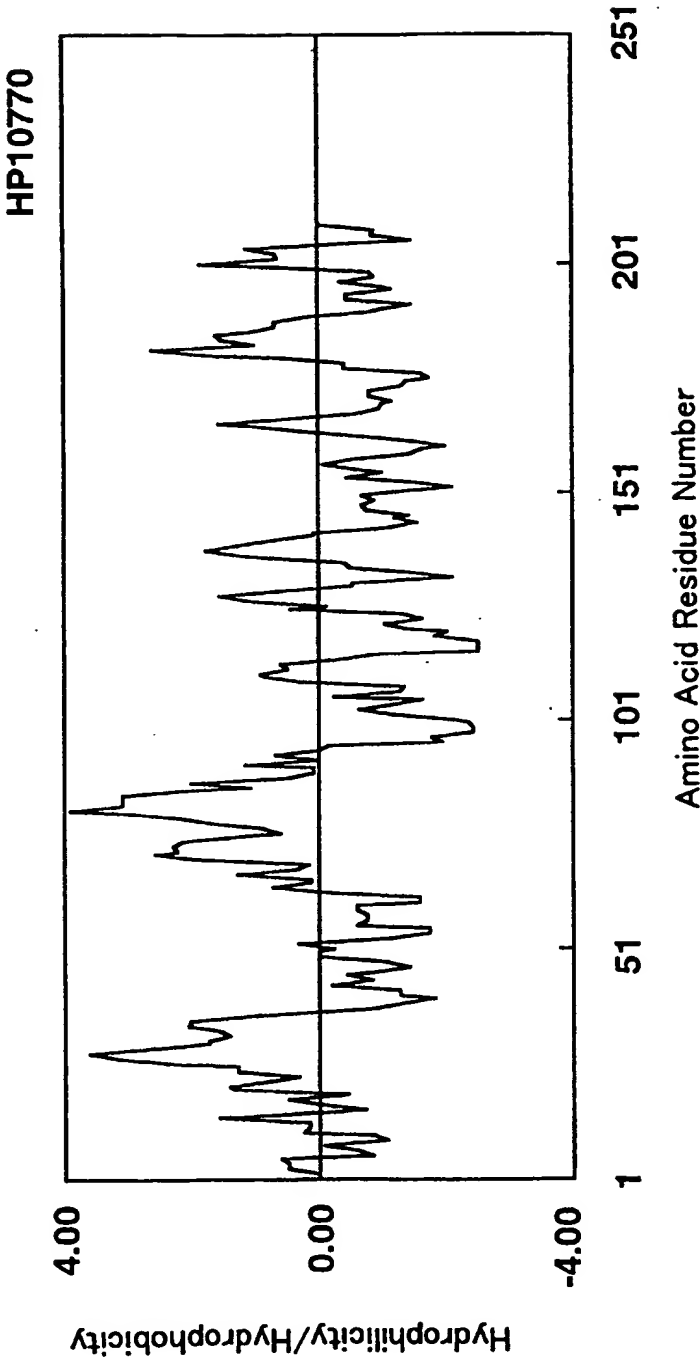


Fig.47

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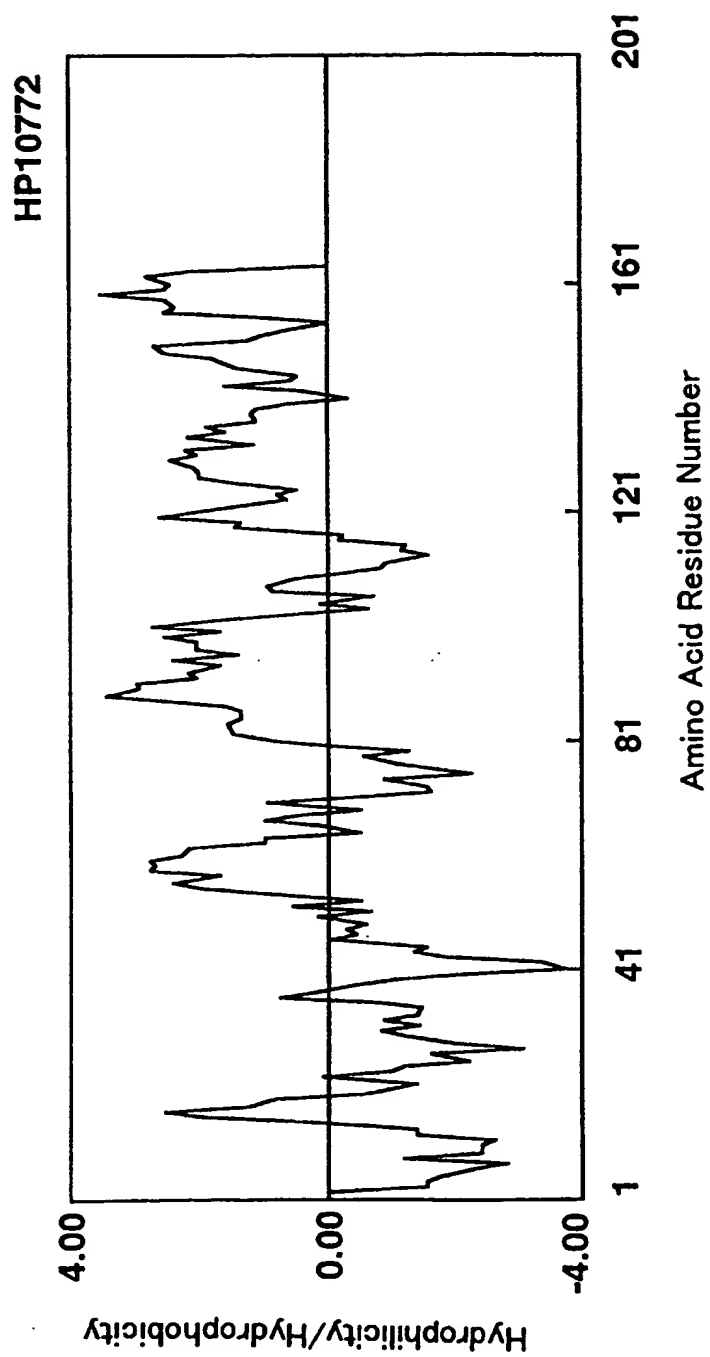


Fig.48

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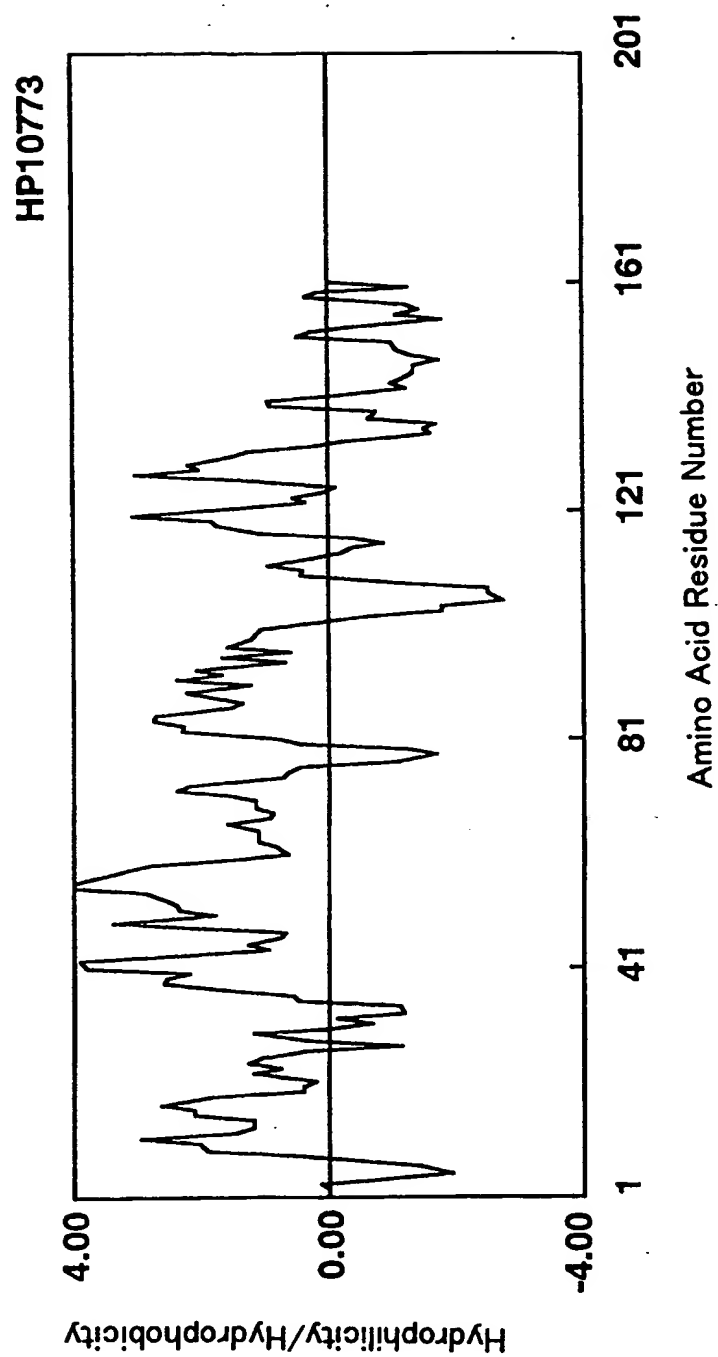


Fig.49

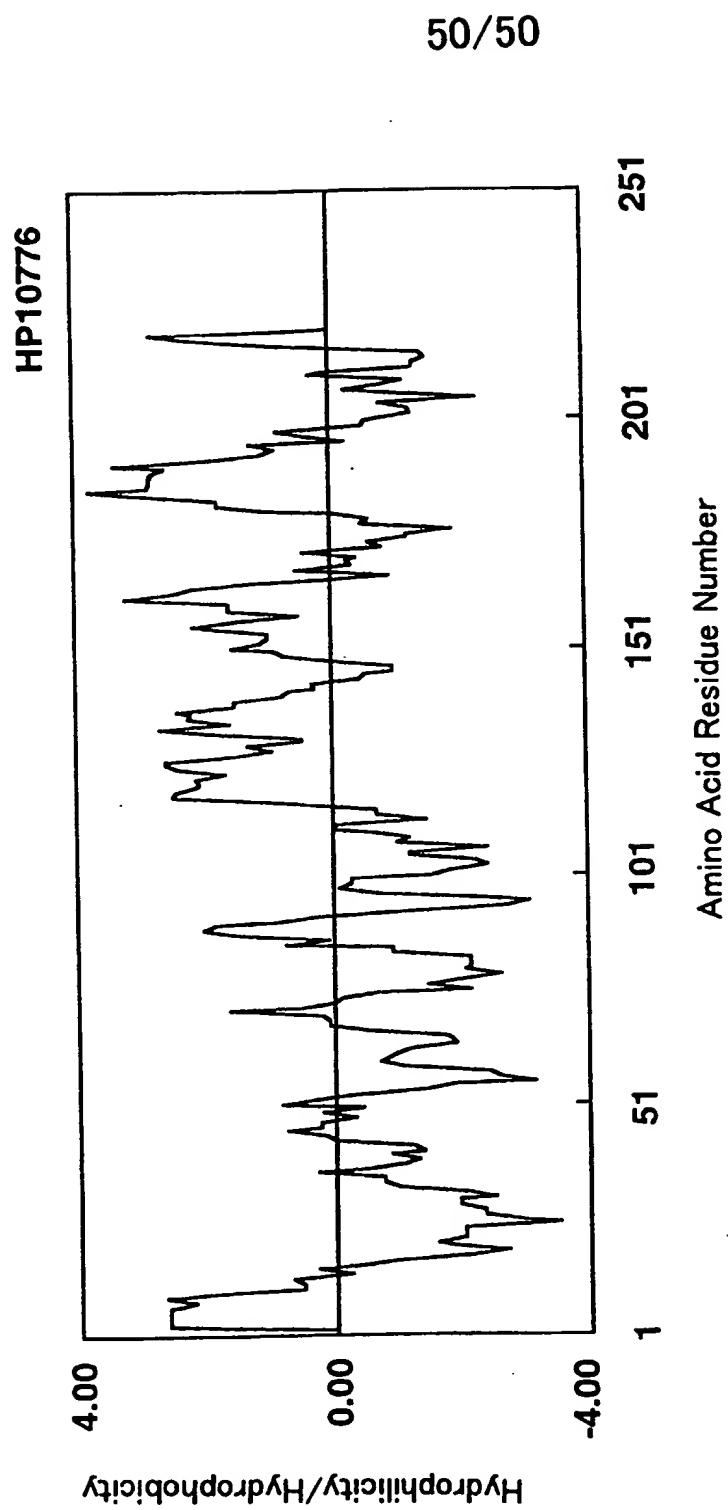


Fig.50

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SEQUENCE LISTING

<110> Sagami Chemical Research Center,
Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these
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<151> 1999-08-17

<150> JP 11-252551

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<150> JP 11-281132

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<151> 1999-11-04

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<160> 150

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<211> 267

<212> PRT

<213> Homo sapiens

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Met Val Lys Ile Ser Phe Gln Pro Ala Val Ala Gly Ile Lys Gly Asp

1 5 10 15

Lys Ala Asp Lys Ala Ser Ala Ser Ala Pro Ala Pro Ala Ser Ala Thr

20 25 30

Glu Ile Leu Leu Thr Pro Ala Arg Glu Glu Gln Pro Pro Gln His Arg

35 40 45

Ser Lys Arg Gly Ser Ser Val Gly Gly Val Cys Tyr Leu Ser Met Gly

50 55 60

Met Val Val Leu Leu Met Gly Leu Val Phe Ala Ser Val Tyr Ile Tyr

65 70 75 80

Arg Tyr Phe Phe Leu Ala Gln Leu Ala Arg Asp Asn Phe Phe Arg Cys

85 90 95

Gly Val Leu Tyr Glu Asp Ser Leu Ser Ser Gln Val Arg Thr Gln Met

100 105 110

Glu Leu Glu Glu Asp Val Lys Ile Tyr Leu Asp Glu Asn Tyr Glu Arg

115 120 125

Ile Asn Val Pro Val Pro Gln Phe Gly Gly Gly Asp Pro Ala Asp Ile

130 135 140

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Ile His Asp Phe Gln Arg Gly Leu Thr Ala Tyr His Asp Ile Ser Leu

145 150 155 160

Asp Lys Cys Tyr Val Ile Glu Leu Asn Thr Thr Ile Val Leu Pro Pro

165 170 175

Arg Asn Phe Trp Glu Leu Leu Met Asn Val Lys Arg Gly Thr Tyr Leu

180 185 190

Pro Gln Thr Tyr Ile Ile Gln Glu Glu Met Val Val Thr Glu His Val

195 200 205

Ser Asp Lys Glu Ala Leu Gly Ser Phe Ile Tyr His Leu Cys Asn Gly

210 215 220

Lys Asp Thr Tyr Arg Leu Arg Arg Arg Ala Thr Arg Arg Arg Ile Asn

225 230 235 240

Lys Arg Gly Ala Lys Asn Cys Asn Ala Ile Arg His Phe Glu Asn Thr

245 250 255

Phe Val Val Glu Thr Leu Ile Cys Gly Val Val

260 265

<210> 2

<211> 419

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala Ala Leu Ala

1 5 10 15

Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala Ser Gln

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20	25	30	
Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val Gln Glu Pro Gly Arg			
35	40	45	
Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly Leu Asp			
50	55	60	
Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu Pro Leu			
65	70	75	80
His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg Phe Phe			
85	90	95	
Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn			
100	105	110	
Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn Ala Val			
115	120	125	
Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val Thr Met			
130	135	140	
Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu Leu			
145	150	155	160
Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln			
165	170	175	
Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg			
180	185	190	
Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile			
195	200	205	
Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr			
210	215	220	

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Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys

225 230 235 240

Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu

245 250 255

Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr Lys

260 265 270

Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His Lys

275 280 285

Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met Cys

290 295 300

Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro Cys

305 310 315 320

Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln Ala

325 330 335

Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser Leu

340 345 350

Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln Asp

355 360 365

Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr Lys

370 375 380

Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr Leu

385 390 395 400

Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu Val

405 410 415

Glu Trp Phe

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<210> 3

<211> 415

<212> PRT

<213> Homo sapiens

<400> 3

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala

1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr

20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly

35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr

50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu

65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly

85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro

100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser

115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala

130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg

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145	150	155	160
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro			
	165	170	175
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu			
	180	185	190
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys			
	195	200	205
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala			
	210	215	220
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val			
	225	230	235
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu			
	245	250	255
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu			
	260	265	270
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr			
	275	280	285
Gly Leu Lys Thr Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr			
	290	295	300
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly			
	305	310	315
Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val			
	325	330	335
Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala			
	340	345	350

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Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro

355

360

365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu

370

375

380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys

385

390

395

400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys

405

410

415

<210> 4

<211> 380

<212> PRT

<213> Homo sapiens

<400> 4

Met Leu Gln Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu

1

5

10

15

Pro Val Asn Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val

20

25

30

Tyr Ala Lys Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu

35

40

45

Phe Leu Ile Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu

50

55

60

Ala Ala Leu Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro

65

70

75

80

Asn Ala Thr Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys

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	85	90	95
Gln Val Glu Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg			
100	105	110	
Gln Val Glu Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser			
115	120	125	
Leu Leu Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu			
130	135	140	
Ile Ala Phe Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe			
145	150	155	160
Tyr Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile			
165	170	175	
Pro Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser			
180	185	190	
Leu Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu			
195	200	205	
Gln Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp			
210	215	220	
Phe Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp			
225	230	235	240
Ser Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly			
245	250	255	
Trp Lys Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe			
260	265	270	
Ile Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr			
275	280	285	

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Leu Val Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe

290 295 300

Phe Asn Ser Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala

305 310 315 320

Tyr Leu Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val

325 330 335

Glu Asp Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu

340 345 350

Glu Ala Ala Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly

355 360 365

His Pro Ile Leu Asn Asn Asn His Arg Lys Asn Asp

370 375 380

<210> 5

<211> 585

<212> PRT

<213> Homo sapiens

<400> 5

Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys Trp Val Phe

1 5 10 15

Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala Ile Val Leu

20 25 30

Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala Cys Ser Pro

35 40 45

Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln Ile Ser Arg

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50	55	60	
Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn Ser Lys Lys			
65	70	75	80
Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu Glu Ala Asp			
	85	90	95
Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly Val Pro Ile			
100	105	110	
Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu Glu Gln Trp			
115	120	125	
Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys Leu Asp Phe			
130	135	140	
Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu Arg Gln Leu			
145	150	155	160
Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn Ala Asp Ile			
	165	170	175
Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn Ala Thr Gln			
180	185	190	
Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr Leu Ser Pro			
195	200	205	
Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg Thr Tyr Thr			
210	215	220	
Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly Val Pro Gln			
225	230	235	240
Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala Ala Trp Pro			
	245	250	255

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His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser Leu Thr Leu

260

265

270

Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu Leu Tyr Val

275

280

285

Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile Phe Glu Pro

290

295

300

Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr Arg Lys Pro

305

310

315

320

Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln Leu Pro Gly

325

330

335

Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val Gln Gly Ser

340

345

350

Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly Met Ile Leu

355

360

365

Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro Val Pro Ile

370

375

380

Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser Cys Leu Gln

385

390

395

400

Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu Gln Ile Ala

405

410

415

Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala Arg Leu Ser

420

425

430

Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala Lys Ile Ser

435

440

445

His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg Glu Leu Leu

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450 455 460
 Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala Pro Gly Trp
 465 470 475 480
 Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu Leu Thr Asp
 485 490 495
 Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser Phe Gln Met
 500 505 510
 Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile Gly Arg Leu
 515 520 525
 Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His Asn Pro Ala
 530 535 540
 Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala Ala Arg Ala
 545 550 555 560
 Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly Tyr His Lys
 565 570 575
 Asp Leu Leu Ala His Val Gly Arg Asn
 580 585

<210> 6

<211> 331

<212> PRT

<213> Homo sapiens

<400> 6

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe

1

5

10

15

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Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 20 25 30
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 35 40 45
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 50 55 60
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
 65 70 75 80
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
 85 90 95
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
 100 105 110
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
 115 120 125
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
 130 135 140
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala
 145 150 155 160
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
 165 170 175
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
 180 185 190
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
 195 200 205
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

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210 215 220
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
 225 230 235 240
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
 245 250 255
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
 260 265 270
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
 275 280 285
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
 290 295 300
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
 305 310 315 320
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 325 330

<210> 7

<211> 345

<212> PRT

<213> Homo sapiens

<400> 7

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile Ser Ile
 1 5 10 15
 Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys Arg Trp
 20 25 30

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Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys Gly Pro

35

40

45

His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala Leu Ile

50

55

60

Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp Thr Phe

65

70

75

80

Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu Pro Thr

85

90

95

Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu Lys Leu

100

105

110

Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln Arg Lys

115

120

125

Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu Leu Pro

130

135

140

Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys Tyr Val

145

150

155

160

Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu Asp Trp

165

170

175

Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro Leu Leu

180

185

190

Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu Leu Ser

195

200

205

Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe Tyr Ala

210

215

220

Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe Phe Ala

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225 230 235 240
Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys Gly Cys
 245 250 255
Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala Arg Ala
 260 265 270
Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro Glu Lys
 275 280 285
Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile Asp Cys
 290 295 300
Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg Tyr Trp
305 310 315 320
Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys Ser Ala
 325 330 335
Pro Ala Arg Ser Tyr Val Leu Arg Leu
 340 345

<210> 8

<211> 89

<212> PRT

<213> Homo sapiens

<400> 8

Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly
1 5 10 15
Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe
20 25 30

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Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp

35

40

45

Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys

50

55

60

Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe

65

70

75

80

Ala Asp Ile Ser Ile Leu Ser Asp Phe

85

<210> 9

<211> 406

<212> PRT

<213> Homo sapiens

<400> 9

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro

1

5

10

15

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

20

25

30

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn

35

40

45

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

50

55

60

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val

65

70

75

80

Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp

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	85	90	95
Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro			
100	105	110	
Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe Thr Arg Leu Leu			
115	120	125	
Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala Lys Pro Leu Gly			
130	135	140	
Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser Trp Asn Asn Ile			
145	150	155	160
Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr Phe Gln Gly His			
165	170	175	
Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly Ser Leu Ala Phe			
180	185	190	
Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala Gln Pro Pro Arg			
195	200	205	
Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val Ala Leu Ile Gly			
210	215	220	
Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu Glu Val Ala Thr			
225	230	235	240
Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu Gln His Ser Ile			
245	250	255	
Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp Gln Leu Leu Trp			
260	265	270	
Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro Val Ala Tyr Ser			
275	280	285	

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Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro

290

295

300

Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg

305

310

315

320

Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe

325

330

335

Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp

340

345

350

Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro

355

360

365

Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met

370

375

380

Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser

385

390

395

400

Glu Tyr Gln Ser Ile Asn

405

<210> 10

<211> 192

<212> PRT

<213> Homo sapiens

<400> 10

Met Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln

1

5

10

15

Pro Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr

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	20	25	30
Cys Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly			
	35	40	45
His Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys			
	50	55	60
Thr Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln			
	65	70	75
Ala His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val			
	85	90	95
Gly Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met			
	100	105	110
Val Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met			
	115	120	125
Gly Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu			
	130	135	140
Leu Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe			
	145	150	155
Thr Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu			
	165	170	175
Asn Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu			
	180	185	190

<210> 11

<211> 801

<212> DNA

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<213> Homo sapiens

<400> 11

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gaggagcagc ccccaaca tcgatccaag agggggagct cagtggcgcg cgtgtgctac	180
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gacaagtgt atgtcatga actcaacacc accattgtgc tgccccctcg caacttctgg	540
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gagatggtgg tcacggagca tgtcagtgc aaggaggccc tggggtcctt catctaccac	660
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acgtcatct gcggggtggt g	801

<210> 12

<211> 1257

<212> DNA

<213> Homo sapiens

<400> 12

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gtgacggtgc aggagcccgg ccgcggcgcc ccgtcacgt ttgcacga ccgcgggcgc	180

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tacgggcttg actccccaa ggccgaggtc cgcggccagg tgctggcgcc gctgcccctc	240
cacggagttg ctgatcatct gggtgtgat ccacaaaccc gggtctttgt ccctccta	300
atcaaacagt ggattgcctt gctgcagagg ggaaactgca cgtttaaaga gaaaatatca	360
cgggcccgtt tccacaatgc agttgctgta gtcactaca ataataaatc caaagaggag	420
ccagttacca tgactcatcc aggcaactga gatattattg ctgtcatgat aacagaattg	480
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<210> 13

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 13

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tctggattta ttggcagtga aggttttcct ggagtgtacc ctccaaatag caaatgtact	180
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cagcgcattg gccgcttctg tggcactttc cggcctggag cccttgtgtc cagtggcaac	360
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caagtaggtg aagatgggag aggcaaaatc atgccaaaca gctttatcat gatgttcaag	1200
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<210> 14

<211> 1140

<212> DNA

<213> Homo sapiens

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<400> 14

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gctacaccac tggctgccct cttgaacata aaggagaaaa ctcggctgcg ggcacctccc	240
aacgccacct tggaacattt ctacctgacc agtggaagc agcccaagca ggtggaagta	300
gagcttttgt cccggcagag cgggtctctt ggccgccagg tagagcgttg gttccgtcgc	360
cgccgcaacc aggaccggcc cagtctctc aagaagttcc gagaagccag ctggagattc	420
acattttacc tgattgcctt cattgccggc atggccgtca ttgtggataa accctggttc	480
tatgacatga agaaagtttg ggagggatat cccatacaga gcactatccc ttcccagtat	540
tggtactaca tgattgaact ttccttctac tggtcctgc tcttcagcat tgcctctgat	600
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<210> 15

<211> 1755

<212> DNA

<213> Homo sapiens

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<400> 15

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tgtgagctgg aggctgcag cctgatgcc gacatgctgg actacctgct gagcctgggc	180
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acagaggaag gcaaagtccg gcggcccata tggatcaacg ctgacatctt aaagggtccc	540
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 cacaaccag ctgggggcga ctatgcctct gtgaggacag cattgctggc agctagggt 1680
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<210> 16

<211> 993

<212> DNA

<213> Homo sapiens

<400> 16

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atgcataata tcttgtggta cctgtgtgga atttcagctt tcctcatgca aaaggatttt 840
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<210> 17

<211> 1035

<212> DNA

<213> Homo sapiens

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tatgtcctgc gcctt 1035

<210> 18

<211> 267

<212> DNA

<213> Homo sapiens

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<210> 19

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 19

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gtgtctctgg aggtcatccc taactggctg ggccccctgc agaacctgct tcatatacgg 180
gcagtgggca ccaattccac actgcactat gtgtggagca gcctggggcc tctggcagtg 240
gtaatgggtg ccaccaacac cccccacagc accctgagcg tcaactggag cctcctgcta 300

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tcccctgagc ccgatggggg cctgatggtg ctccctaagg acagcattca gttttcttct	360
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<210> 20

<211> 576

<212> DNA

<213> Homo sapiens

<400> 20

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tcctcggtct ccatttgtga tgggcactgg ctcttggtg aggaccgcct ctccgggtc	180

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 gcccatgtgc cgggctggc cgtgggcatg ggcctggtag gcagcgtggg cgccttggcc 300
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<210> 21

<211> 2042

<212> DNA

<213> Homo sapiens

<220>

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<222> (91)... (894)

<400> 21

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Met Val Lys Ile Ser Phe Gln

1

5

ccc gcc gtg gct ggc atc aag ggc gac aag gct gac aag gcg tcg gcg 159

Pro Ala Val Ala Gly Ile Lys Gly Asp Lys Ala Asp Lys Ala Ser Ala

10

15

20

tcg gcc cct gcg ccg gcc tcg gcc acc gag atc ctg ctg acg ccg gct 207

Ser Ala Pro Ala Pro Ala Ser Ala Thr Glu Ile Leu Leu Thr Pro Ala

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25	30	35	
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Arg Glu Glu Gln Pro Pro Gln His Arg Ser Lys Arg Gly Ser Ser Val			
40	45	50	55
ggc ggc gtg tgc tac ctg tcg atg ggc atg gtc gtg ctg ctc atg ggc			303
Gly Gly Val Cys Tyr Leu Ser Met Gly Met Val Val Leu Leu Met Gly			
60	65	70	
ctc gtg ttc gcc tct gtc tac atc tac aga tac ttc ttt ctt gca cag			351
Leu Val Phe Ala Ser Val Tyr Ile Tyr Arg Tyr Phe Phe Leu Ala Gln			
75	80	85	
ctg gcc cga gat aac ttc ttc cgc tgt ggt gtg ctg tat gag gac tcc			399
Leu Ala Arg Asp Asn Phe Phe Arg Cys Gly Val Leu Tyr Glu Asp Ser			
90	95	100	
ctg tcc tcc cag gtc cgg act cag atg gag ctg gaa gag gat gtg aaa			447
Leu Ser Ser Gln Val Arg Thr Gln Met Glu Leu Glu Glu Asp Val Lys			
105	110	115	
atc tac ctc gac gag aac tac gag cgc atc aac gtg cct gtg ccc cag			495
Ile Tyr Leu Asp Glu Asn Tyr Glu Arg Ile Asn Val Pro Val Pro Gln			
120	125	130	135
ttt ggc ggc ggt gac cct gca gac atc atc cat gac ttc cag cgg ggt			543
Phe Gly Gly Gly Asp Pro Ala Asp Ile Ile His Asp Phe Gln Arg Gly			
140	145	150	
ctg act gcg tac cat gat atc tcc ctg gac aag tgc tat gtc atc gaa			591
Leu Thr Ala Tyr His Asp Ile Ser Leu Asp Lys Cys Tyr Val Ile Glu			
155	160	165	

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etc aac acc acc att gtg ctg ccc cct cgc aac ttc tgg gag etc etc 639
 Leu Asn Thr Thr Ile Val Leu Pro Pro Arg Asn Phe Trp Glu Leu Leu
 170 175 180
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 Met Asn Val Lys Arg Gly Thr Tyr Leu Pro Gln Thr Tyr Ile Ile Gln
 185 190 195
 gag gag atg gtg gtc acg gag cat gtc agt gac aag gag gcc ctg ggg 735
 Glu Glu Met Val Val Thr Glu His Val Ser Asp Lys Glu Ala Leu Gly
 200 205 210 215
 tcc ttc atc tac cac ctg tgc aac ggg aaa gac acc tac cgg ctc cgg 783
 Ser Phe Ile Tyr His Leu Cys Asn Gly Lys Asp Thr Tyr Arg Leu Arg
 220 225 230
 cgc cgg gca acg cgg agg cgg atc aac aag cgt ggg gcc aag aac tgc 831
 Arg Arg Ala Thr Arg Arg Arg Ile Asn Lys Arg Gly Ala Lys Asn Cys
 235 240 245
 aat gcc atc cgc cac ttc gag aac acc ttc gtg gtg gag acg ctc atc 879
 Asn Ala Ile Arg His Phe Glu Asn Thr Phe Val Val Glu Thr Leu Ile
 250 255 260
 tgc ggg gtg gtg tgaggccctc ctccccaga accccctgcc gtgttctc 930
 Cys Gly Val Val
 265
 tttttttttt tccggtgct ctctggccct cctccttccc cctgcttagc ttgtactttg 990
 gacgcgtttc tatagaggtg acatgtctct ccattcctct ccaaccctgc ccacctccct 1050
 gtaccagagc tgtgatctct cgggtgggggg cccatctctg ctgacctggg tgtggcggag 1110
 ggagaggcga tgctgcaaag tgttttctgt gtcccactgt cttgaagctg ggcctgcca 1170

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agcctgggcc cacagctgca ccggcagccc aagggaagg accggttggg ggagccgggc 1230
 atgtgaggcc ctgggcaagg ggatggggct gtgggggcgg ggcgcatgg gcttcagaag 1290
 tatctgcaca attagaaaag tcctcagaag ctttttcttg gaggtacac tttcttact 1350
 gtccctatc ctagacctgg ggcttgagct gaggatggga cgatgtgcc agggaggagc 1410
 ccaccagagc acaagagaag gtggtacct gggggtgtcc cagggactct gtcagtgcct 1470
 tcagcccacc agcaggagct tggagtttg ggagtgggga tgagtccgtc aagcacaact 1530
 gttctctgag tggaacaaaa gaagcaagga gctaggacct ccagtcctgc ccccaggag 1590
 cacaagcagg gtccctcag tcaaggcagt gggatgggcg gctgaggaac ggggcaggca 1650
 aggtcactgc tcagtcacgt ccacggggga cgagccgtgg gttctgctga gtaggtggag 1710
 ctcattgctt tctccaagct tggaactgtt ttgaaagata acacagagg aaaggagag 1770
 ccacctggta ctgtccacc ctgcctctc tgtctgaaa ttccatcccc ctcagcttag 1830
 gggaatgcac ctttttcct ttccttctca cttttgcatg ttttactga tcattcgata 1890
 tgctaaccgt tctcagccct gagccttga gaggagggt gtaacgcctt cagtcagtct 1950
 ctggggatga aactcttaaa tgctttgtat attttctcaa ttagatctct tttcagaagt 2010
 gtctatagaa caataaaaat cttttacttc tg 2042

<210> 22

<211> 1433

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (5)... (1264)

<400> 22

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Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala Ala

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1	5	10	
ctc gcc ctg ctg acc tgc agc ctg tgg ccg gca cgg gca gac aac gcg			94
Leu Ala Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala			
15	20	25	30
agc cag gag tac tac acg gcg ctc atc aac gtg acg gtg cag gag ccc			142
Ser Gln Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val Gln Glu Pro			
35	40	45	
ggc cgc ggc gcc ccg ctc acg ttt cgc atc gac cgc ggg cgc tac ggg			190
Gly Arg Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly			
50	55	60	
ctt gac tcc ccc aag gcc gag gtc cgc ggc cag gtg ctg gcg ccg ctg			238
Leu Asp Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu			
65	70	75	
ccc ctc cac gga gtt gct gat cat ctg ggc tgt gat cca caa acc cgg			286
Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg			
80	85	90	
ttc ttt gtc cct cct aat atc aaa cag tgg att gcc ttg ctg cag agg			334
Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg			
95	100	105	110
gga aac tgc acg ttt aaa gag aaa ata tca cgg gcc gct ttc cac aat			382
Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn			
115	120	125	
gca gtt gct gta gtc atc tac aat aat aaa tcc aaa gag gag cca gtt			430
Ala Val Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val			
130	135	140	

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acc atg act cat cca ggc act gga gat att att gct gtc atg ata aca	478
Thr Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr	
145 150 155	
gaa ttg agg ggt aag gat att ttg agt tat ctg gag aaa aac atc tct	526
Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser	
160 165 170	
gta caa atg aca ata gct gtt gga act cga atg cca ccg aag aac ttc	574
Val Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe	
175 180 185 190	
agc cgt ggc tct cta gtc ttc gtg tca ata tcc ttt att gtt ttg atg	622
Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met	
195 200 205	
att att tct tca gca tgg ctc ata ttc tac ttc att cag aag atc agg	670
Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg	
210 215 220	
tac aca aat gca cgc gac agg aac cag cgt cgt ctc gga gat gca gcc	718
Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala	
225 230 235	
aag aaa gcc atc agt aaa ttg aca acc agg aca gta aag aag ggt gac	766
Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp	
240 245 250	
aag gaa act gac cca gac ttt gat cat tgt gca gtc tgc ata gag agc	814
Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser	
255 260 265 270	
tat aag cag aat gat gtc gtc cga att ctc ccc tgc aag cat gtt ttc	862

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Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe	
275 280 285	
cac aaa tcc tgc gtg gat ccc tgg ctt agt gaa cat tgt acc tgt cct	910
His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro	
290 295 300	
atg tgc aaa ctt aat ata ttg aag gcc ctg gga att gtg ccg aat ttg	958
Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu	
305 310 315	
cca tgt act gat aac gta gca ttc gat atg gaa agg ctc acc aga acc	1006
Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr	
320 325 330	
caa gct gtt aac cga aga tca gcc ctc ggc gac ctc gcc ggc gac aac	1054
Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn	
335 340 345 350	
tcc ctt ggc ctt gag cca ctt cga act tcg ggg atc tca cct ctt cct	1102
Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro	
355 360 365	
cag gat ggg gag ctc act ccg aga aca gga gaa atc aac att gca gta	1150
Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val	
370 375 380	
aca aaa gaa tgg ttt att att gcc agt ttt ggc ctc ctc agt gcc ctc	1198
Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu	
385 390 395	
aca ctc tgc tac atg atc atc aga gcc aca gct agc ttg aat gct aat	1246
Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn	

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400 405 410

gag gta gaa tgg ttt tgaagaagaa aaaacctgct ttctgactga ttttgcctt 1300

Glu Val Glu Trp Phe

415

gaaggaaaaa agaacctatt tttgtgcatc atttaccaat catgccacac aagcatttat 1360

ttttagtaca ttttattttt tcataaaatt gctaatacca aagctttgta ttaaaagaaa 1420

taaataataa aat 1433

<210> 23

<211> 1917

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)... (1457)

<400> 23

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cagccgagcg ccggtgtgag ccagcgctgc tgccagtgtg agccagcgct gctgccagtg 120

tgagcgcgcg tgtgagcgcg gtgggtgcgg aggggctgtg gtgccggcgc gcgcgcccgtg 180

gggtgcaaac cccgagcgtc tacgtgcc atg agg ggc gcg aac gcc tgg gcg 233

Met Arg Gly Ala Asn Ala Trp Ala

1

5

cca etc tgc ctg ctg ctg gct gcc gcc acc cag etc tcg cgg cag cag 281

Pro Leu Cys Leu Leu Leu Ala Ala Ala Thr Gln Leu Ser Arg Gln Gln

10

15

20

tcc cca gag aga cct gtt ttc aca tgt ggt ggc att ctt act gga gag	329
Ser Pro Glu Arg Pro Val Phe Thr Cys Gly Gly Ile Leu Thr Gly Glu	
25 30 35 40	
tct gga ttt att ggc agt gaa ggt ttt cct gga gtg tac cct cca aat	377
Ser Gly Phe Ile Gly Ser Glu Gly Phe Pro Gly Val Tyr Pro Pro Asn	
45 50 55	
agc aaa tgt act tgg aaa atc aca gtt ccc gaa gga aaa gta gtc gtt	425
Ser Lys Cys Thr Trp Lys Ile Thr Val Pro Glu Gly Lys Val Val Val	
60 65 70	
ctc aat ttc cga ttc ata gac ctc gag agt gac aac ctg tgc cgc tat	473
Leu Asn Phe Arg Phe Ile Asp Leu Glu Ser Asp Asn Leu Cys Arg Tyr	
75 80 85	
gac ttt gtg gat gtg tac aat ggc cat gcc aat ggc cag cgc att ggc	521
Asp Phe Val Asp Val Tyr Asn Gly His Ala Asn Gly Gln Arg Ile Gly	
90 95 100	
cgc ttc tgt ggc act ttc cgg cct gga gcc ctt gtg tcc agt ggc aac	569
Arg Phe Cys Gly Thr Phe Arg Pro Gly Ala Leu Val Ser Ser Gly Asn	
105 110 115 120	
aag atg atg gtg cag atg att tct gat gcc aac aca gct ggc aat ggc	617
Lys Met Met Val Gln Met Ile Ser Asp Ala Asn Thr Ala Gly Asn Gly	
125 130 135	
ttc atg gcc atg ttc tcc gct gct gaa cca aac gaa aga ggg gat cag	665
Phe Met Ala Met Phe Ser Ala Ala Glu Pro Asn Glu Arg Gly Asp Gln	
140 145 150	
tat tgt gga gga ctc ctt gac aga cct tcc ggc tct ttt aaa acc ccc	713

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Tyr Cys Gly Gly Leu Leu Asp Arg Pro Ser Gly Ser Phe Lys Thr Pro
 155 160 165
 aac tgg cca gac cgg gat tac cct gca gga gtc act tgt gtg tgg cac 761
 Asn Trp Pro Asp Arg Asp Tyr Pro Ala Gly Val Thr Cys Val Trp His
 170 175 180
 att gta gcc cca aag aat cag ctt ata gaa tta aag ttt gag aag ttt 809
 Ile Val Ala Pro Lys Asn Gln Leu Ile Glu Leu Lys Phe Glu Lys Phe
 185 190 195 200
 gat gtg gag cga gat aac tac tgc cga tat gat tat gtg gct gtg ttt 857
 Asp Val Glu Arg Asp Asn Tyr Cys Arg Tyr Asp Tyr Val Ala Val Phe
 205 210 215
 aat ggc ggg gaa gtc aac gat gct aga aga att gga aag tat tgt ggt 905
 Asn Gly Gly Glu Val Asn Asp Ala Arg Arg Ile Gly Lys Tyr Cys Gly
 220 225 230
 gat agt cca cct gcg cca att gtg tct gag aga aat gaa ctt ctt att 953
 Asp Ser Pro Pro Ala Pro Ile Val Ser Glu Arg Asn Glu Leu Leu Ile
 235 240 245
 cag ttt tta tca gac tta agt tta act gca gat ggg ttt att ggt cac 1001
 Gln Phe Leu Ser Asp Leu Ser Leu Thr Ala Asp Gly Phe Ile Gly His
 250 255 260
 tac ata ttc agg cca aaa aaa ctg cct aca act aca gaa cag cct gtc 1049
 Tyr Ile Phe Arg Pro Lys Lys Leu Pro Thr Thr Thr Glu Gln Pro Val
 265 270 275 280
 acc acc aca ttc cct gta acc acg ggt tta aaa acc acc gtg gcc ttg 1097
 Thr Thr Thr Phe Pro Val Thr Thr Gly Leu Lys Thr Thr Val Ala Leu

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285	290	295	
tgt caa caa aag tgt aga cgg acg ggg act ctg gag ggc aat tat tgt			1145
Cys Gln Gln Lys Cys Arg Arg Thr Gly Thr Leu Glu Gly Asn Tyr Cys			
300	305	310	
tca agt gac ttt gta tta gcc ggc act gtt atc aca acc atc act cgc			1193
Ser Ser Asp Phe Val Leu Ala Gly Thr Val Ile Thr Thr Ile Thr Arg			
315	320	325	
gat ggg agt ttg cac gcc aca gtc tgc atc atc aac atc tac aaa gag			1241
Asp Gly Ser Leu His Ala Thr Val Ser Ile Ile Asn Ile Tyr Lys Glu			
330	335	340	
gga aat ttg gcg att cag cag gcg ggc aag aac atg agt gcc agg ctg			1289
Gly Asn Leu Ala Ile Gln Gln Ala Gly Lys Asn Met Ser Ala Arg Leu			
345	350	355	360
act gtc gtc tgc aag cag tgc cct ctc ctc aga aga ggt cta aat tac			1337
Thr Val Val Cys Lys Gln Cys Pro Leu Leu Arg Arg Gly Leu Asn Tyr			
365	370	375	
att att atg ggc caa gta ggt gaa gat ggg cga ggc aaa atc atg cca			1385
Ile Ile Met Gly Gln Val Gly Glu Asp Gly Arg Gly Lys Ile Met Pro			
380	385	390	
aac agc ttt atc atg atg ttc aag acc aag aat cag aag ctc ctg gat			1433
Asn Ser Phe Ile Met Met Phe Lys Thr Lys Asn Gln Lys Leu Leu Asp			
395	400	405	
gcc tta aaa aat aag caa tgt taacagtga ctgtgtccat ttaagc			1480
Ala Leu Lys Asn Lys Gln Cys			
410	415		

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tgtattctgc cattgccttt gaaagatcta tgttctctca gtagaaaaaa aaatacttat 1540
 aaaattacat attctgaaag aggattccga aagatgggac tggttgactc ttcacatgat 1600
 ggaggtatga ggccctccgag atagctgagg gaagttcttt gcctgctgtc agaggagcag 1660
 ctatctgatt ggaaacctgc cgacttagtg cggatgatagg aagctaaaag tgtcaagcgt 1720
 tgacagcttg gaagcgttta tttatacatc tctgtaaaag gatatttttag aattgagttg 1780
 tgtgaagatg tcaaaaaaag attttagaag tgcaatattt atagtgttat ttgtttcacc 1840
 ttcaagcctt tgccctgagg tgttacaatc ttgtcttgcg ttttctaaat caatgcttaa 1900
 taaaatattt ttaaagg 1917

<210> 24

<211> 2258

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)... (1367)

<400> 24

tttttcccg ctgggctcgg gctcagctcg actgggctcg gcgggcggcg gcggcggcgc 60
 ccgcggcttg cggaggaggg agggcgaggg cgggcgcggg ccggcgggcg ggcggaagag 120
 ggaggagagg cgcggggagc caggcctcgg ggccctcgag caaccacccg agcagacgga 180
 gtacacggag cagcggcccc ggccccgcca acgctgccgc cggg atg etc cag 233

Met Leu Gln

1

acc ttg tat gat tac ttc tgg tgg gaa cgt ctg tgg ctg cct gtg aac 281

Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu Pro Val Asn

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5	10	15	
ttg acc tgg gcc gat cta gaa gac cga gat gga cgt gtc tac gcc aaa	329		
Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val Tyr Ala Lys			
20	25	30	35
gcc tca gat ctc tat atc acg ctg ccc ctg gcc ttg ctc ttc ctc atc	377		
Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu Phe Leu Ile			
40	45	50	
gtt cga tac ttc ttt gag ctg tac gtg gct aca cca ctg gct gcc ctc	425		
Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu Ala Ala Leu			
55	60	65	
ttg aac ata aag gag aaa act cgg ctg cgg gca cct ccc aac gcc acc	473		
Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro Asn Ala Thr			
70	75	80	
ttg gaa cat ttc tac ctg acc agt ggc aag cag ccc aag cag gtg gaa	521		
Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys Gln Val Glu			
85	90	95	
gta gag ctt ttg tcc cgg cag agc ggg ctc tct ggc cgc cag gta gag	569		
Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg Gln Val Glu			
100	105	110	115
cgt tgg ttc cgt cgc cgc cgc aac cag gac cgg ccc agt ctc ctc aag	617		
Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser Leu Leu Lys			
120	125	130	
aag ttc cga gaa gcc agc tgg aga ttc aca ttt tac ctg att gcc ttc	665		
Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu Ile Ala Phe			
135	140	145	

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att gcc ggc atg gcc gtc att gtg gat aaa ccc tgg ttc tat gac atg	713
Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met	
150 155 160	
aag aaa gtt tgg gag gga tat ccc ata cag agc act atc cct tcc cag	761
Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln	
165 170 175	
tat tgg tac tac atg att gaa ctt tcc ttc tac tgg tcc ctg ctc ttc	809
Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe	
180 185 190 195	
agc att gcc tct gat gtc aag cga aag gat ttc aag gaa cag atc atc	857
Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile	
200 205 210	
cac cat gtg gcc acc atc att ctc atc agc ttt tcc tgg ttt gcc aat	905
His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn	
215 220 225	
tac atc cga gct ggg act cta atc atg gct ctg cat gac tct tcc gat	953
Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp	
230 235 240	
tac ctg ctg gag tca gcc aag atg ttt aac tac gcg gga tgg aag aac	1001
Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn	
245 250 255	
acc tgc aac aac atc ttc atc gtc ttc gcc att gtt ttt atc atc acc	1049
Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe Ile Ile Thr	
260 265 270 275	
cga ctg gtc atc ctg ccc ttc tgg atc ctg cat tgc acc ctg gtg tac	1097

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Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr Leu Val Tyr
 280 285 290
 cca ctg gag ctc tat cct gcc ttc ttt ggc tat tac ttc ttc aat tcc 1145
 Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe Phe Asn Ser
 295 300 305
 atg atg gga gtt cta cag ctg ctg cat atc ttc tgg gcc tac ctc att 1193
 Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala Tyr Leu Ile
 310 315 320
 ttg cgc atg gcc cac aag ttc ata act gga aag ctg gta gaa gat gaa 1241
 Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val Glu Asp Glu
 325 330 335
 cgc agt gac cgg gaa gaa aca gag agc tca gag ggg gag gag gct gca 1289
 Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu Glu Ala Ala
 340 345 350 355
 gct ggg gga gga gca aag agc cgg ccc cta gcc aat ggc cac ccc atc 1337
 Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly His Pro Ile
 360 365 370
 ctc aat aac aac cat cgt aag aat gac tgaaccatta ttccagctgc ctccca 1390
 Leu Asn Asn Asn His Arg Lys Asn Asp
 375 380
 gattaatgca taaagccaag gaactaccct gctccctgcg ctatagggtc actttaagct 1450
 ctggggaaaa aggagaaagt gagaggagag ttctctgcat cctccctcct tgcttgccac 1510
 ccagttgcct ttaaaccaaa ttctaaccag cctatcccca ggtaggggga cggttggttat 1570
 attctgttag agggggacgg tcgtattttc ctccctaccc gccaaagtcac cctttctact 1630
 gcttttgagg cctccctca gctctctgtg ggtaggggtt acaattcaca ttccttattc 1690

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tgagaatttg gccccagctg ttgaccttg actccctgac ctccagagcc agggttgtgc 1750
 cttattgtcc catctgtggg cctcattctg ccaaagctgg accaaggcta acctttctaa 1810
 gctccctaac ttgggccaga aaccaaagct gagcttttaa ctttctccct ctatgacaca 1870
 aatgaattga gggtaggagg agggcgcaca taacccttac cctacctctg ccaaaaagtg 1930
 ggggctgtac tggggactgc tcggatgac tttcttagtg ctacttcttt cagctgtccc 1990
 tgtagcgaca ggtctaagat ctgactgcct ctttctctg gcctcttccc ctttccctct 2050
 tctcttcagc taggctagct gggttgagtg agaattggca ctaattctaa tttttattta 2110
 ttaaatattt ggggttttgg ttttaaagcc agaattacgg ctacaccta gcatttcagc 2170
 agagggacca ttttagacca aaatgtactg ttaatgggtt tttttttaa attaaaagat 2230
 taaataaaaa atattaaata aaacatgg 2258

<210> 25

<211> 1973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (130)... (1887)

<400> 25

gagcagacca gggccggtgg agaattaggt gctgctggga gctcctgcct cccacaggat 60
 tccagctgca gggagcctca gggactctgg gccgcacgga gttgggggca ttccccagag 120
 agcgtcgcc atg gtc tgc agg gag cag tta tca aag aat cag gtc aag 168

Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys

1

5

10

tgg gtg ttt gcc ggc att acc tgt gtg tct gtg gtg gtc att gcc gca 216

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Trp Val Phe Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala
 15 20 25
 ata gtc ctt gcc atc acc ctg cgg cgg cca ggc tgt gag ctg gag gcc 264
 Ile Val Leu Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala
 30 35 40 45
 tgc agc cct gat gcc gac atg ctg gac tac ctg ctg agc ctg ggc cag 312
 Cys Ser Pro Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln
 50 55 60
 atc agc cgg cga gat gcc ttg gag gtc acc tgg tac cac gca gcc aac 360
 Ile Ser Arg Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn
 65 70 75
 agc aag aaa gcc atg aca gct gcc ctg aac agc aac atc aca gtc ctg 408
 Ser Lys Lys Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu
 80 85 90
 gag gct gac gtc aat gta gaa ggg ctc ggc aca gcc aat gag aca gga 456
 Glu Ala Asp Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly
 95 100 105
 gtt ccc atc atg gca cac ccc ccc act atc tac agt gac aac aca ctg 504
 Val Pro Ile Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu
 110 115 120 125
 gag cag tgg ctg gac gct gtg ctg ggc tct tcc caa aag ggc atc aaa 552
 Glu Gln Trp Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys
 130 135 140
 ctg gac ttc aag aac atc aag gca gtg ggc ccc tcc ctg gac ctc ctg 600
 Leu Asp Phe Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu

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145	150	155	
cgg cag ctg aca gag gaa ggc aaa gtc cgg cgg ccc ata tgg atc aac			648
Arg Gln Leu Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn			
160	165	170	
gct gac atc tta aag ggc ccc aac atg ctc atc tca act gag gtc aat			696
Ala Asp Ile Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn			
175	180	185	
gcc aca cag ttc ctg gcc ctg gtc cag gag aag tat ccc aag gct acc			744
Ala Thr Gln Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr			
190	195	200	205
cta tct cca ggc tgg acc acc ttc tac atg tcc acg tcc cca aac agg			792
Leu Ser Pro Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg			
210	215	220	
acg tac acc caa gcc atg gtg gag aag atg cac gag ctg gtg gga gga			840
Thr Tyr Thr Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly			
225	230	235	
gtg ccc cag agg gtc acc ttc cct gta cgg tct tcc atg gtg cgg gct			888
Val Pro Gln Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala			
240	245	250	
gcc tgg ccc cac ttc agc tgg ctg ctg agc caa tct gag agg tac agc			936
Ala Trp Pro His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser			
255	260	265	
ctg acg ctg tgg cag gct gcc tcg gac ccc atg tcg gtg gaa gat ctg			984
Leu Thr Leu Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu			
270	275	280	285

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ctc tac gtc cgg gat aac act gct gtc cac caa gtc tac tat gac atc	1032
Leu Tyr Val Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile	
290 295 300	
ttt gag cct ctc ctg tca cag ttc aag cag ctg gcc ttg aat gcc aca	1080
Phe Glu Pro Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr	
305 310 315	
cgg aaa cca atg tac tac aca gga ggc agc ctg atc cct ctt ctc cag	1128
Arg Lys Pro Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln	
320 325 330	
ctg cct ggg gat gac ggt ctg aat gtg gag tgg ctg gtt cct gac gtc	1176
Leu Pro Gly Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val	
335 340 345	
cag ggc agc ggt aaa aca gca aca atg acc ctc cca gac aca gaa ggc	1224
Gln Gly Ser Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly	
350 355 360 365	
atg atc ctg ctg aac act ggc ctc gag gga act gtg gct gaa aac ccc	1272
Met Ile Leu Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro	
370 375 380	
gtg ccc att gtt cat act cca agt ggc aac atc ctg acg ctg gag tcc	1320
Val Pro Ile Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser	
385 390 395	
tgc ctg cag cag ctg gcc aca cat ccc gga cac tgg ggc atc cat ttg	1368
Cys Leu Gln Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu	
400 405 410	
caa ata gcg gag ccc gca gcc ctc cgg cca tcc ctg gcc ttg ctg gca	1416

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Gln Ile Ala Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala
 415 420 425
 cgc ctc tcc agc ctt ggc ctc ttg cat tgg cct gtg tgg gtt ggg gcc 1464
 Arg Leu Ser Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala
 430 435 440 445
 aaa atc tcc cac ggg agt ttt tcg gtc ccc ggc cat gtg gct ggc aga 1512
 Lys Ile Ser His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg
 450 455 460
 gag ctg ctt aca gct gtg gct gag gtc ttc ccc cac gtg act gtg gca 1560
 Glu Leu Leu Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala
 465 470 475
 cca ggc tgg cct gag gag gtg ctg ggc agt ggc tac agg gaa cag ctg 1608
 Pro Gly Trp Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu
 480 485 490
 ctc aca gat atg cta gag ttg tgc cag ggg ctc tgg caa cct gtg tcc 1656
 Leu Thr Asp Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser
 495 500 505
 ttc cag atg cag gcc atg ctg ctg ggc cac agc aca gct gga gcc ata 1704
 Phe Gln Met Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile
 510 515 520 525
 ggc agg ctg ctg gca tcc tcc ccc cgg gcc acc gtc aca gtg gag cac 1752
 Gly Arg Leu Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His
 530 535 540
 aac cca gct ggg ggc gac tat gcc tct gtg agg aca gca ttg ctg gca 1800
 Asn Pro Ala Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala

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545	550	555	
gct agg gct gtg gac agg acc cga gtc tac tac agg cta ccc cag ggc			1848
Ala Arg Ala Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly			
560	565	570	
tac cac aag gac ttg ctg gct cat gtt ggt aga aac tgagcaccca ggggtg			1900
Tyr His Lys Asp Leu Leu Ala His Val Gly Arg Asn			
575	580	585	
gtgggccagc ggacctcagg gcggaggctt cccacgggga ggcaggaaga aataaagtc			1960
tttgctttc tcc			1973

<210> 26

<211> 1606

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (135)... (1130)

<400> 26

attgtgcggc gctggtcccc tcagagggtt cctgctgctg ccggtgcctt ggacctcccc	60
cctcgcttct cgttctactg ccccaggagc cggcggggtc cgggactccc gtccgtgccg	120
gtgcggggcg cggc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc	170

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly

1

5

10

cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg	218
Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro	

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15	20	25	
gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc			266
Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val			
30	35	40	
ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag			314
Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys			
45	50	55	60
ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac			362
Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp			
65	70	75	
gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga			410
Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly			
80	85	90	
gca aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct			458
Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro			
95	100	105	
gtc tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg			506
Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly			
110	115	120	
cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca			554
Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala			
125	130	135	140
gca aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc			602
Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr			
145	150	155	

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cta agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc	650
Leu Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe	
160 165 170	
ttt gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa	698
Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys	
175 180 185	
atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct	746
Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser	
190 195 200	
ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta	794
Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val	
205 210 215 220	
ata aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat	842
Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp	
225 230 235	
ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg	890
Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met	
240 245 250	
atg gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg	938
Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu	
255 260 265	
tgt gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc	986
Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala	
270 275 280	
tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act	1034

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Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr
 285 290 295 300
 gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc 1082
 Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser
 305 310 315
 agc tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc 1127
 Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 320 325 330
 tag actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatac 1180
 agggatatca aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca 1240
 aatgcaatag ttggtcactg catttttacc tgaaccaaag ctaaaccggt tgttgccacc 1300
 atgcaccatg gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa 1360
 cgcacaagag cccctgcctt gccctagctg aggcacacag ggagaccag tgaggataag 1420
 cacagattga attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcattgataa 1480
 ctcagagttg acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt 1540
 taacatgtac tgtagacatc aaacttgtgg ccatactaataaaaattatta aaaggagcac 1600
 taaagg 1606

<210> 27

<211> 2380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (247)... (1284)

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<400> 27

agtgtggacc tggactcgaa tcccgttgcc gactcgcgct ctcggttct gctccggggc 60
 ttcttcctg cccgcccggg gccctgacg tggtttctt cccggcctga tctgcgcagc 120
 ccggcgggcg ccagaaagga gcaggcggcg cggggcgcg ctgggcgggg gaggcgtggc 180
 cggagctgcg gcggcaagcg ggctgggact gctcggccgc ctctgcccg gcgagcagct 240
 cagacc atg tcg cct gaa gaa tgg acg tat cta gtg gtt ctt ctt atc 288

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile

1 5 10

tcc atc ccc atc ggc ttc ctc ttt aag aaa gcc ggt cct ggg ctg aag 336

Ser Ile Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys

15 20 25 30

aga tgg gga gca gcc gct gtg ggc ctg ggg ctc acc ctg ttc acc tgt 384

Arg Trp Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys

35 40 45

ggc ccc cac act ttg cat tct ctg gtc acc atc ctc ggg acc tgg gcc 432

Gly Pro His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala

50 55 60

ctc att cag gcc cag ccc tgc tcc tgc cac gcc ctg gct ctg gcc tgg 480

Leu Ile Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp

65 70 75

act ttc tcc tat ctc ctg ttc ttc cga gcc ctc agc ctc ctg ggc ctg 528

Thr Phe Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu

80 85 90

ccc act ccc acg ccc ttc acc aat gcc gtc cag ctg ctg ctg acg ctg 576

Pro Thr Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu

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95	100	105	110	
aag ctg gtg agc ctg gcc agt gaa gtc cag gac ctg cat ctg gcc cag				624
Lys Leu Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln				
	115	120	125	
agg aag gaa atg gcc tca ggc ttc agc aag ggg ccc acc ctg ggg ctg				672
Arg Lys Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu				
	130	135	140	
ctg ccc gac gtg ccc tcc ctg atg gag aca ctc agc tac agc tac tgc				720
Leu Pro Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys				
	145	150	155	
tac gtg gga atc atg aca ggc ccg ttc ttc cgc tac cgc acc tac ctg				768
Tyr Val Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu				
	160	165	170	
gac tgg ctg gag cag ccc ttc ccc ggg gca gtg ccc agc ctg cgg ccc				816
Asp Trp Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro				
	175	180	185	190
ctg ctg cgc cgc gcc tgg ccg gcc ccg ctc ttc ggc ctg ctg ttc ctg				864
Leu Leu Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu				
	195	200	205	
ctc tcc tct cac ctc ttc ccg ctg gag gcc gtg cgc gag gac gcc ttc				912
Leu Ser Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe				
	210	215	220	
tac gcc cgc ccg ctg ccc gcc cgc ctc ttc tac atg atc ccc gtc ttc				960
Tyr Ala Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe				
	225	230	235	

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ttc gcc ttc cgc atg cgc ttc tac gtg gcc tgg att gcc gcc gag tgc	1008
Phe Ala Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys	
240 245 250	
ggc tgc att gcc gcc ggc ttt ggg gcc tac ccc gtg gcc gcc aaa gcc	1056
Gly Cys Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala	
255 260 265 270	
cgg gcc gga ggc gcc ccc acc ctc caa tgc cca ccc ccc agc agt ccg	1104
Arg Ala Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro	
275 280 285	
gag aag gcg gct tcc ttg gag tat gac tat gag acc atc cgc aac atc	1152
Glu Lys Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile	
290 295 300	
gac tgc tac agc aca gat ttc tgc gtg cgg gtg cgc gat ggc atg cgg	1200
Asp Cys Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg	
305 310 315	
tac tgg aac atg acg gtg cag tgg tgg ctg gcg cag tat atc tac aag	1248
Tyr Trp Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys	
320 325 330	
agc gca cct gcc cgt tcc tat gtc ctg cgc ctt tagaagcaga aactcagcc	1300
Ser Ala Pro Ala Arg Ser Tyr Val Leu Arg Leu	
335 340 345	
gggtgcggcg gctcacgcct ggaatcccag cactttggga ggccaagca ggtggatcat	1360
gaggagcgcc tggaccatgc tgctgagcgc ctactggcac ggctccacc cgggctacta	1420
cctgagcttc ctgaccatcc cgctgtgcct ggctgccgag ggccggctgg agtcagccct	1480
gcgggggagg ctgagcccag ggggccagaa ggctgggac tgggtgcact ggttcctgaa	1540

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gatgcgcgcc tatgactaca tgtgcatggg ctctccttgg ccgacaccct 1600
 tcgggtactgg gcctccatct acttctgtat ccacttcctg gccctggcag ccctggggct 1660
 ggggcttgct ttaggtgggg gcagccccag ccggcggaag gcagcatccc agcccaccag 1720
 ccttgccccg gagaagctcc gggaggagta agctgtcag acgtccctc tgccagctgg 1780
 tcccgggaat tctgtgaacc aggtgtgtgt ctctcccca gaaagagtcc ttaccttga 1840
 gagggtcctg gagagaattt cctcttcccc agctaaatac cctgcctgca actgaagcag 1900
 acccggggggt gtcctccctg ccctctgccc agaggccacc tccactccta caaaatcaaa 1960
 gtattgtcca gacaagagtc actggccctt gctccagctt ctgggtatcc agagagcact 2020
 gcacttcccc aaaacggaag gggcccttgg gcagtgggtt ttgggcaaat tccctttctt 2080
 tgcattccaca atgtggggtc ggagcttggg ggcaggtcct gggagtggga agcctcttcc 2140
 ttgtgtcttt cgtccactt ttagctcctc gcaccaatat tgcagacttg gaaggaagca 2200
 taagcttccc atttcacaaa ggggaaactg aggtgcgggt gcgcgggcct ggggacggcc 2260
 gtcccatggc ttccatctga gccacctcgg gaccccagca ctcttgccgc cctcttctca 2320
 tcgcttgccc tatgacaggt caccgtgtgt aaatctttcc caataaagtg ttgcacaaag 2380

<210> 28

<211> 2017

<212> DNA

<213> Homo. sapiens

<220>

<221> CDS

<222> (360)... (629)

<400> 28

tccacacatt aagaaacgct ggtggagttt taaatgcctc tccggggaag gaggaaagcc 60
 tgagaatgaa tctgacctca gaccacaaatc cattcaacgg agttctggta atttgaaga 120

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aggaagagca acctggaaac tgacaggaaa ggatgacaag ttgggagtca caggatatatg	180
atgggcctcc ccatgtggat ccttagtgct gtggcagagc ccttggtatt gtgctgggat	240
tttcctcca gctcccgcc ggaagctggg ctcacgtggg agtcagtgc ctcctgcta	300
cagatctgtc tcttccttac aatgggggtgc tggcactgtg ggtcctgggtg acgcacgtg	359
atg tac atg caa gat tat tgg agg acc tgg ctc aag ggg ctg cgc ggc	407
Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly	
1 5 10 15	
ttc ttc ttc gtg ggc gtc ctc ttc tgc gcc gtc tcc atc gct gcc ttc	455
Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe	
20 25 30	
tgc acc ttc ctc gtg ctg gcc atc acc cgg cat cag agc ctc aca gac	503
Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp	
35 40 45	
ccc acc agc tac tac ctc tcc agc gtc tgg agc ttc att tcc ttc aag	551
Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys	
50 55 60	
tgg gcc ttc ctg ctc agc ctc tat gcc cac cgc tac cgg gct gac ttt	599
Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe	
65 70 75 80	
gct gac atc agc atc ctc agc gat ttc tgaccaggg ggtg	640
Ala Asp Ile Ser Ile Leu Ser Asp Phe	
85	
aggtctctgc accctggggg ggccttagga cctggactca gcctctgaga tgttgggaga	700
ggctactccc acccctggt gacccagaa ctgtggcaga aaatacacag caggacgagt	760
gtggtctccc aggaagctgt cctgccgctc ccttttcgag gaaacctgag tgtggtagag	820

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aggggatcct gccatgttgt tcctcatcag cctggccaga gggcagcttt agaccttttc 880
aatgaatct gttttctttt ctttcttttt tttttctttt tttttttttt ttgagatgga 940
gtcttactct gtcaccagg ctggagtga gtagtgcat ctcagctcac tgcaacctcc 1000
gcctcccagg ttcaagcaat tctcctgcct tggcctctca agtagctggg attacaggca 1060
tctgccacca tgcccggcaa atttttgtgt ttttagtaga gacagggttt tgccatgttg 1120
gccaggtgg tctcgaactc ctgatctcag gtgattcacc cgcctcagcc ttcaaagtg 1180
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aggcctggac ctatgtgca ggcaagggtt tccatccccg ctgcctagg cactctcttc 1360
ccaaggccag gttgggcacc tggggaggtc agttcagaaa tatctagcag agacctctta 1420
aaccacctc ccagacccc atcctgttgt tcccagagct ggtctcccat gagtgtgcta 1480
gagccagata gccgtggccc cccacctc tcaactcac acacaggcat ccatacccc 1540
cagaagactt cccaaatgag gccagactca gggtcacggg gaatgtgctt ctgccctgt 1600
aagggtttg gggaaggggg caacatagta gaggtggaa agagcccca aacctgtgcc 1660
catgccctc cagccctgcg tttccattct gccttctcag agtgcccttg ctgcaccag 1720
accaccggcc aggagagacc ttctctccca ctccagcccc tctactgcc cttcaactag 1780
agctttcacc tttttacatt tcccttctga aggacacaaa tctgcttttc tgccataca 1840
ctggcccaag ggtcaccta acttgggagg gaaggggctg ttgtacaag gatgattttc 1900
tgtagactg ccattttgca cggctctccc ctcccatct gatgtgtcct gccctcagc 1960
tctttgcctt atctgtgtca ctgtcacttt agcaaaaata cagcgccat ttgtatc 2017

<210> 29

<211> 1606

<212> DNA

<213> Homo sapiens

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<220>

<221> CDS

<222> (30)... (1250)

<400> 29

acctcttccg tcggctgaat tgcggccgt atg cgc ggc tct gtg gag tgc acc	53
Met Arg Gly Ser Val Glu Cys Thr	
1 5	
tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta	101
Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu	
10 15 20	
ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag	149
Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln	
25 30 35 40	
gtg tct ctg gag gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg	197
Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu	
45 50 55	
ctt cat ata cgg gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg	245
Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp	
60 65 70	
agc agc ctg ggg cct ctg gca gtg gta atg gtg gcc acc aac acc ccc	293
Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro	
75 80 85	
cac agc acc ctg agc gtc aac tgg agc ctc ctg cta tcc cct gag ccc	341
His Ser Thr Leu Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro	
90 95 100	

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gat ggg ggc ctg atg gtg ctc cct aag gac agc att cag ttt tct tct	389
Asp Gly Gly Leu Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser	
105 110 115 120	
gcc ctt gtt ttt acc agg ctg ctt gag ttt gac agc acc aac gtg tcc	437
Ala Leu Val Phe Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser	
125 130 135	
gat acg gca gca aag cct ttg gga aga cca tat cct cca tac tcc ttg	485
Asp Thr Ala Ala Lys Pro Leu Gly Arg Pro Tyr Pro Pro Tyr Ser Leu	
140 145 150	
gcc gat ttc tct tgg aac aac atc act gat tca ttg gat cct gcc acc	533
Ala Asp Phe Ser Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr	
155 160 165	
ctg agt gcc aca ttt caa ggc cac ccc atg aac gac cct acc agg act	581
Leu Ser Ala Thr Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr	
170 175 180	
ttt gcc aat ggc agc ctg gcc ttc agg gtc cag gcc ttt tcc agg tcc	629
Phe Ala Asn Gly Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser	
185 190 195 200	
agc cga cca gcc caa ccc cct cgc ctc ctg cac aca gca gac acc tgt	677
Ser Arg Pro Ala Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys	
205 210 215	
cag cta gag gtg gcc ctg att gga gcc tct ccc cgg gga aac cgt tcc	725
Gln Leu Glu Val Ala Leu Ile Gly Ala Ser Pro Arg Gly Asn Arg Ser	
220 225 230	
ctg ttt ggg ctg gag gta gcc aca ttg ggc cag ggc cct gac tgc ccc	773

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Leu Phe Gly Leu Glu Val Ala Thr Leu Gly Gln Gly Pro Asp Cys Pro
 235 240 245
 tca atg cag gag cag cac tcc atc gac gat gaa tat gca ccg gcc gtc 821
 Ser Met Gln Glu Gln His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val
 250 255 260
 ttc cag ttg gac cag cta ctg tgg ggc tcc ctc cca tca ggc ttt gca 869
 Phe Gln Leu Asp Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala
 265 270 275 280
 cag tgg cga cca gtg gct tac tcc cag aag ccg ggg ggc cga gaa tca 917
 Gln Trp Arg Pro Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser
 285 290 295
 gcc ctg ccc tgc caa gct tcc cct ctt cat cct gcc tta gca tac tct 965
 Ala Leu Pro Cys Gln Ala Ser Pro Leu His Pro Ala Leu Ala Tyr Ser
 300 305 310
 ctt ccc cag tca ccc att gtc cga gcc ttc ttt ggg tcc cag aat aac 1013
 Leu Pro Gln Ser Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn
 315 320 325
 ttc tgt gcc ttc aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat 1061
 Phe Cys Ala Phe Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr
 330 335 340
 tgg gac caa cac tac ctc agc tgg tcg atg ctc ctg ggt gtg ggc ttc 1109
 Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe
 345 350 355 360
 cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg 1157
 Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val

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365	370	375	
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg			1205
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu			
380	385	390	
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat taa			1250
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn			
395	400	405	
ggccccgtct ctggagggaa ggacattact gaacctgtct tgctgtgcct cgaaactctg			1310
gaggttgag catcaagttc cagccggccc cttactccc ccatcttgct tttctgtgga			1370
acctcagagg ccagcctcga cttcctggag acccccaggt ggggcttcct tcatactttg			1430
ttgggggact ttggaggcgg gcaggggaca gggctattga taaggcccc ttggtgttgc			1490
cttcttgcat ctccacacat ttcccttgga tgggacttgc aggcctaaat gagaggcatt			1550
ctgactgggt ggctgccctg gaaggcaaga aaatagattt attttttttc acaggg			1606

<210> 30

<211> 1695

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)... (631)

<400> 30

acagccgagc agctggagcg atcgaggctg cagcgcggcc gccgggcgca gc atg	55
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Met

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act gcc gtc ggc gtg cag gcc cag agg cct ttg ggc caa agg cag ccc	103
Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln Pro	
5 10 15	
cgc cgg tcc ttc ttt gaa tcc ttc atc cgg acc ctc atc atc acg tgt	151
Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr Cys	
20 25 30	
gtg gcc ctg gct gtg gtc ctg tcc tcg gtc tcc att tgt gat ggg cac	199
Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly His	
35 40 45	
tgg ctc ctg gct gag gac cgc ctc ttc ggg ctc tgg cac ttc tgc acc	247
Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys Thr	
50 55 60 65	
acc acc aac cag agt gtg ccg atc tgc ttc aga gac ctg ggc cag gcc	295
Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln Ala	
70 75 80	
cat gtg ccc ggg ctg gcc gtg ggc atg ggc ctg gta cgc agc gtg ggc	343
His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val Gly	
85 90 95	
gcc ttg gcc gtg gtg gcc gcc att ttt ggc ctg gag ttc ctc atg gtg	391
Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met Val	
100 105 110	
tcc cag ttg tgc gag gac aaa cac tca cag tgc aag tgg gtc atg ggt	439
Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met Gly	
115 120 125	
tcc atc ctc ctc ctg gtg tct ttc gtc ctc tcc tcc ggc ggg ctc ctg	487

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Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu Leu
 130 135 140 145
 ggt ttt gtg atc ctc ctc agg aac caa gtc aca ctc atc ggc ttc acc 535
 Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe Thr
 150 155 160
 cta atg ttt tgg tgc gaa ttc act gcc tcc ttc ctc ctc ttc ctg aac 583
 Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu Asn
 165 170 175
 gcc atc agc ggc ctt cac atc aac agc atc acc cat ccc tgg gaa tg 630
 Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu
 180 185 190
 accgtgga aa ttttaggcc cctccaggga catcagattc cacaagaaaa tatggtcaaa 690
 atgggacttt tccagcatgt ggcctctggt ggggctgggt tggacaaggg ccttgaaacg 750
 gctgcctgtt tgccgataac ttgtgggtgg tcagccagaa atggcccggg ggcctctgca 810
 cctggtctgc agggccagag gccaggaggg tgcctcagt ccaccaactg cacaggctta 870
 gccagatgtt gattttagag gaagaaaaaa acattttaaa actccttctt gaattttctt 930
 ccctggactg gaatacagtt ggaagcacag gggttaactg tacctgagct agctgcacag 990
 ccaaggatag ttcatgcctg ttccattgac acgtgctggg ataggggctg cagaatccct 1050
 ggggctccca ggggtgttaa gaatgatca ttcttcagc taagggtcca atcagtgcct 1110
 attcttcac cagctcaaag ggccttcgta tgtatgtccc tggttcagc tttggtcatg 1170
 ccaaagaggc agagttcagg attccctcag aatgccctgc acacagtagg tttccaaacc 1230
 attgactcg gtttgctcc ctgcccgtt tttaaacctt acaaaccctg gataacccca 1290
 tcttctagca gctggctgtc cctctggga gctctgcta tcagaaccct accttaaggt 1350
 gggtttcctt ccgagaagag ttcttgagca agctctccca ggagggccca cctgactgct 1410
 aatacacagc cctccccaag gcccggtgtg gcatgtgtct gtcttttgtg agggttagac 1470

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agcctcaggg caccattttt aatcccagaa cacatttcaa agagcacgta tctagacctg 1530
 ctggactctg cagggggtga gggggaacag cgagagcttg ggtaatgatt aacacccatg 1590
 ctgggggatgc atggaggtga agggggccag gaaccagtgg agatttccat ccttgccagc 1650
 acgtctgtac ttctgttcat taaagtgtc cctttctagt ccttt 1695

<210> 31

<211> 377

<212> PRT

<213> Homo sapiens

<400> 31

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly

1 5 10 15

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile

20 25 30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe

35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser

50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile

65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe

85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu

100 105 110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe

68 /307

115	120	125	
Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln			
130	135	140	
Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr			
145	150	155	160
Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr			
165	170	175	
Leu Leu Arg Lys His Trp Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe			
180	185	190	
Ser Leu Asn Gly Val Glu Leu Leu His Leu Asn Asn Val Ser Thr Gly			
195	200	205	
Cys Ile Leu Leu Gly Gly Leu Phe Ile Tyr Asp Val Phe Trp Val Phe			
210	215	220	
Gly Thr Asn Val Met Val Thr Val Ala Lys Ser Phe Glu Ala Pro Ile			
225	230	235	240
Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn			
245	250	255	
Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val Ile Pro Gly Ile Phe			
260	265	270	
Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu Lys Lys Asn Thr His			
275	280	285	
Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu			
290	295	300	
Thr Ile Phe Ile Met His Ile Phe Lys His Ala Gln Pro Ala Leu Leu			
305	310	315	320

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Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val Leu Val Ala Leu Ala

325

330

335

Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys

340

345

350

Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala

355

360

365

Ser Lys Gly Leu Glu Lys Lys Glu Lys

370

375

<210> 32

<211> 81

<212> PRT

<213> Homo sapiens

<400> 32

Met Thr Ala His Ser Phe Ala Leu Pro Val Ile Ile Phe Thr Thr Phe

1

5

10

15

Trp Gly Leu Val Gly Ile Ala Gly Pro Trp Phe Val Pro Lys Gly Pro

20

25

30

Asn Arg Gly Val Ile Ile Thr Met Leu Val Ala Thr Ala Val Cys Cys

35

40

45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe

50

55

60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Val Arg Phe Leu Trp

65

70

75

80

Glu

71 / 307

Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala Ala Ile Leu

145 150 155 160

Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly Ser Tyr Val

165 170 175

Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala Ile Ile Ile

180 185 190

Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys Asn Phe Asp

195 200 205

Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile Ser Leu Ala

210 215 220

Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln Leu Asn Tyr

225 230 235 240

Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro Leu Ala Ile

245 250 255

Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu Met Asn Val

260 265 270

Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln Ser Gln Ala

275 280 285

Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala Ser Trp Ile

290 295 300

Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala Asn Gly Thr

305 310 315 320

Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg Glu Gly His

325 330 335

Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu Thr Pro Ala

72 /307

340 345 350
Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr Ile Ile Pro
355 360 365
Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala Ala Trp Leu
370 375 380
Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg Phe Thr Arg
385 390 395 400
Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile Pro Val Leu
405 410 415
Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile Ile Ser Lys
420 425 430
Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu Ser Gly Leu
435 440 445
Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp Ala Gln Lys
450 455 460
Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met Glu Val Val
465 470 475 480
Pro Pro Glu Glu Asp Pro Glu
485

<210> 34

<211> 375

<212> PRT

<213> Homo sapiens

<400> 34

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Met Thr Pro Gln Pro Ala Gly Pro Pro Asp Gly Gly Trp Gly Trp Val
 1 5 10 15
 Val Ala Ala Ala Ala Phe Ala Ile Asn Gly Leu Ser Tyr Gly Leu Leu
 20 25 30
 Arg Ser Leu Gly Leu Ala Phe Pro Asp Leu Ala Glu His Phe Asp Arg
 35 40 45
 Ser Ala Gln Asp Thr Ala Trp Ile Ser Ala Leu Ala Leu Ala Val Gln
 50 55 60
 Gln Ala Ala Ser Pro Val Gly Ser Ala Leu Ser Thr Arg Trp Gly Ala
 65 70 75 80
 Arg Pro Val Val Met Val Gly Gly Val Leu Ala Ser Leu Gly Phe Val
 85 90 95
 Phe Ser Ala Phe Ala Ser Gly Leu Leu His Leu Tyr Leu Gly Leu Gly
 100 105 110
 Leu Leu Ala Gly Phe Gly Trp Ala Leu Val Phe Ala Pro Ala Leu Gly
 115 120 125
 Thr Leu Ser Arg Tyr Phe Ser Arg Arg Arg Val Leu Ala Val Gly Leu
 130 135 140
 Ala Leu Thr Gly Asn Gly Ala Ser Ser Leu Leu Leu Ala Pro Ala Leu
 145 150 155 160
 Gln Leu Leu Leu Asp Thr Phe Gly Trp Arg Gly Ala Leu Leu Leu Leu
 165 170 175
 Gly Ala Ile Thr Leu His Leu Thr Pro Cys Gly Ala Leu Leu Leu Pro
 180 185 190
 Leu Val Leu Pro Gly Asp Pro Pro Ala Pro Pro Arg Ser Pro Leu Ala

74 / 307

195	200	205
Ala Leu Gly Leu Ser Leu Phe Thr Arg Arg Ala Phe Ser Ile Phe Ala		
210	215	220
Leu Gly Thr Ala Leu Val Gly Gly Gly Tyr Phe Val Pro Tyr Val His		
225	230	235
Leu Ala Pro Arg Phe Arg Pro Gly Pro Gly Gly Ile Arg Ser Ser Ala		
245	250	255
Gly Gly Gly Arg Gly Cys Asp Gly Gly Cys Gly Arg Pro Ala Gly Leu		
260	265	270
Arg Val Ala Gly Arg Pro Arg Leu Gly Ala Pro Pro Ala Ala Ala Gly		
275	280	285
Arg Ile Arg Gly Ser Asp Trp Ala Gly Ala Val Gly Gly Gly Ala Gly		
290	295	300
Ala Arg Gly Gly Arg Arg Arg Glu Leu Gly Gly Ser Pro Ala Gly Arg		
305	310	315
Gly Cys Gly Leu Trp Ala Glu Arg Gly Glu Leu Arg Pro Ala Gly Phe		
325	330	335
Arg Cys Thr Pro Arg Ala Gly Gly Arg Arg Arg Cys Gly Ala Gly His		
340	345	350
Arg Ala Gly Asp Asp Ala Asp Glu Pro Arg Gly Ala Pro Gly Pro Ser		
355	360	365
Pro Val Arg Leu Pro Lys Gly		
370	375	

75 /307

<211> 350

<212> PRT

<213> Homo sapiens

<400> 35

Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly

1 5 10 15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala

20 25 30

Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu

35 40 45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala

50 55 60

Asp Ala Ala Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu

65 70 75 80

Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln

85 90 95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr

100 105 110

Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln

115 120 125

Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn

130 135 140

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val

145 150 155 160

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr

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165	170	175	
Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe			
180	185	190	
Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu			
195	200	205	
Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr			
210	215	220	
Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His			
225	230	235	240
Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser			
245	250	255	
Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr			
260	265	270	
Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe			
275	280	285	
Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu			
290	295	300	
Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg			
305	310	315	320
Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu			
325	330	335	
Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His			
340	345	350	

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<211> 667

<212> PRT

<213> Homo sapiens

<400> 36

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu
1 5 10 15
Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Glu
20 25 30
Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro
35 40 45
Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu
50 55 60
Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys
65 70 75 80
Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly
85 90 95
Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser
100 105 110
Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr
115 120 125
Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly
130 135 140
Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala Ala Leu Tyr Tyr Pro
145 150 155 160
Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly

78 /307

165	170	175	
Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala			
180	185	190	
Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr Tyr Ser Leu Leu Ala			
195	200	205	
Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu Ser Leu Trp Tyr Pro			
210	215	220	
Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr Gly Ala Gly Ser Lys			
225	230	235	240
Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu Arg Asn Leu Leu Cys			
245	250	255	
Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser Lys His Gly Phe Leu			
260	265	270	
Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile Tyr Thr Pro Gln Pro			
275	280	285	
Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser Ala Thr Leu Thr Gly			
290	295	300	
Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu Val Gly Val Val Pro			
305	310	315	320
Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr Asp Val Ser Tyr Leu			
325	330	335	
Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp Lys Gln Glu Val Val			
340	345	350	
Glu Leu Val Lys His His Leu Trp Ala Leu Glu Val Cys Tyr Ile Ser			
355	360	365	

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Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser

370

375

380

Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu His Arg Gly Ala Ala

385

390

395

400

Leu Asp Leu Ser Pro Leu His Arg Ser Pro His Pro Ser Arg Gln Ala

405

410

415

Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln Thr Ala Phe Ile Cys

420

425

430

Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr Thr Ala

435

440

445

Leu Ala Phe Leu Val Leu Met Pro Val Leu His Gly Arg Asn Leu Leu

450

455

460

Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe Trp Leu Thr Leu Ala

465

470

475

480

Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe Leu Glu

485

490

495

Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu Tyr Ala

500

505

510

Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala Met Val

515

520

525

Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr Asn Ala Ile His Leu

530

535

540

Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg Ala Ala Thr Leu Asp

545

550

555

560

Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln

80 / 307

565	570	575	
Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln			
580	585	590	
Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro			
595	600	605	
Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met			
610	615	620	
Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly Arg Ala Arg Trp Gly			
625	630	635	640
Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys			
645	650	655	
Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro			
660	665		

<210> 37

<211> 464

<212> PRT

<213> Homo sapiens

<400> 37

Met Ile Val Cys Leu Leu Phe Met Met Ile Leu Leu Ala Lys Glu Val
1 5 10 15
Gln Leu Val Asp Gln Thr Asp Ser Pro Leu Leu Ser Leu Leu Gly Gln
20 25 30
Thr Ser Ser Leu Ser Trp His Leu Val Asp Ile Val Ser Tyr Gln Ser
35 40 45

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Val Leu Ser Tyr Phe Ser Ser His Tyr Pro Pro Ser Ile Ile Leu Ala
50 55 60
Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys Leu Leu Lys Val Ser Ala
65 70 75 80
Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys His Leu Asp Ala Val Pro
85 90 95
Lys Cys Gln Ala Phe Thr His Gln Met Val Gln Phe Leu Ser Thr Leu
100 105 110
Glu Gln Asn Gly Lys Ile Thr Leu Ala Val Leu Glu Gln Glu Met Ser
115 120 125
Lys Leu Leu Asp Asp Ile Ile Val Phe Asn Pro Pro Asp Met Asp Ser
130 135 140
Gln Thr Arg His Met Ala Leu Ser Ser Leu Phe Met Glu Val Leu Met
145 150 155 160
Met Met Asn Asn Ala Thr Ile Pro Thr Ala Glu Phe Leu Arg Gly Ser
165 170 175
Ile Arg Thr Trp Ile Gly Gln Lys Met His Gly Leu Val Val Leu Pro
180 185 190
Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala Ser Val Arg His Met Ala
195 200 205
Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr Phe Lys Glu Ser Pro Leu
210 215 220
Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu Val Ser Leu Gln Val Pro
225 230 235 240
Glu Leu Thr Met Glu Glu Phe Leu Gln Glu Cys Leu Thr Leu Gly Ser

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245	250	255	
Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln Cys Leu Asn Ser Glu Gln			
260	265	270	
Thr Leu Arg Asn Glu Met Lys Val Leu Leu Ile Leu Ser Lys Trp Leu			
275	280	285	
Glu Gln Val Tyr Pro Ser Ser Val Glu Glu Glu Ala Lys Leu Phe Leu			
290	295	300	
Trp Trp His Gln Val Leu Gln Leu Ser Leu Ile Gln Thr Glu Gln Asn			
305	310	315	320
Asp Ser Val Leu Thr Glu Ser Val Ile Arg Ile Leu Leu Leu Val Gln			
325	330	335	
Ser Arg Gln Asn Leu Val Ala Glu Glu Arg Leu Ser Ser Gly Ile Leu			
340	345	350	
Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro Leu Ser Asn Arg Phe Arg			
355	360	365	
Val Val Ala Arg Ser Met Ala Ala Phe Leu Ser Val Gln Val Pro Met			
370	375	380	
Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser Glu Leu His Leu Thr Pro			
385	390	395	400
Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu Ser Met Ala Ser Ser Lys			
405	410	415	
Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu Gln Ala Thr Gln Phe Ile			
420	425	430	
Arg His Pro Gly His Cys Leu Gln Asp Gly Lys Ser Phe Leu Ala Leu			
435	440	445	

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Leu Val Asn Cys Leu Tyr Pro Glu Val His Tyr Leu Asp His Ile Arg

450

455

460

<210> 38

<211> 470

<212> PRT

<213> Homo sapiens

<400> 38

Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu

1

5

10

15

Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser

20

25

30

Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro

35

40

45

Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met

50

55

60

Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro

65

70

75

80

Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

85

90

95

Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg

100

105

110

Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys

115

120

125

His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Phe Pro Phe

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130 135 140
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
145 150 155 160
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
165 170 175
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
180 185 190
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
195 200 205
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
210 215 220
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
225 230 235 240
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys
245 250 255
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser
260 265 270
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys
275 280 285
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly
290 295 300
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp
305 310 315 320
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu
325 330 335

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Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val

340

345

350

Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu

355

360

365

Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys

370

375

380

Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu

385

390

395

400

Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe

405

410

415

Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly

420

425

430

Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro

435

440

445

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu

450

455

460

Glu Val Ile Leu Arg Asp

465

470

<210> 39

<211> 243

<212> PRT

<213> Homo sapiens

<400> 39

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro Val Asn Val Phe

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Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly Ile Phe Leu Gly			
35	40	45	
Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile Lys Tyr Gln Gly			
50	55	60	
Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro Val Leu Leu Ser			
65	70	75	80
Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys Phe Lys Met Leu			
85	90	95	
Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val Pro Asp Ser Glu			
100	105	110	
Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly Ile Asn Gln Pro			
115	120	125	
Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile Pro Pro Pro Tyr			
130	135	140	
Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr Leu Gln Ser Val			
145	150	155	160
Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala Ala Ala Ala Met			
165	170	175	
Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln Asp Asn Ser Ala			
180	185	190	
Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp Gly Gly Asn His			
195	200	205	

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Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr Gln Leu Glu Glu

210

215

220

Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu Glu Ile Tyr Ser

225

230

235

240

Leu Pro Arg

<210> 40

<211> 270

<212> PRT

<213> Homo sapiens

<400> 40

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1

5

10

15

Asp Glu Ala Ser Cys Cys Arg Trp Gly Ala Gln His Ala Gly Ala Arg

20

25

30

Glu Leu Ala Ala Leu Tyr Ser Pro Gly Lys Arg Leu Gln Glu Trp Cys

35

40

45

Ser Val Ile Leu Cys Phe Ser Leu Ile Ala His Asn Leu Val His Leu

50

55

60

Leu Leu Leu Ala Arg Trp Glu Asp Thr Pro Leu Val Ile Leu Gly Val

65

70

75

80

Val Ala Gly Ala Leu Ile Ala Asp Phe Leu Ser Gly Leu Val His Trp

85

90

95

Gly Ala Asp Thr Trp Gly Ser Val Glu Leu Pro Ile Val Gly Lys Ala

100

105

110

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Phe Ile Arg Pro Phe Arg Glu His His Ile Asp Pro Thr Ala Ile Thr

115

120

125

Arg His Asp Phe Ile Glu Thr Asn Gly Asp Asn Cys Leu Val Thr Leu

130

135

140

Leu Pro Leu Leu Asn Met Ala Tyr Lys Phe Arg Thr His Ser Pro Glu

145

150

155

160

Ala Leu Glu Gln Leu Tyr Pro Trp Glu Cys Phe Val Phe Cys Leu Ile

165

170

175

Ile Phe Gly Thr Phe Thr Asn Gln Ile His Lys Trp Ser His Thr Tyr

180

185

190

Phe Gly Leu Pro Arg Trp Val Thr Leu Leu Gln Asp Trp His Val Ile

195

200

205

Leu Pro Arg Lys His His Arg Ile His His Val Ser Pro His Glu Thr

210

215

220

Tyr Phe Cys Ile Thr Thr Gly Trp Leu Asn Tyr Pro Leu Glu Lys Ile

225

230

235

240

Gly Phe Trp Arg Arg Leu Glu Asp Leu Ile Gln Gly Leu Thr Gly Glu

245

250

255

Lys Pro Arg Ala Asp Asp Met Lys Trp Ala Gln Lys Ile Lys

260

265

270

<210> 41

<211> 1131

<212> DNA

<213> Homo sapiens

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<400> 41

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<210> 42

<211> 243

<212> DNA

<213> Homo sapiens

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<400> 42

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<210> 43

<211> 1461

<212> DNA

<213> Homo sapiens

<400> 43

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<210> 44

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 44

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 gccagcggtc tgctgcatct ctacctggc ctgggcctcc tcgtggctt tggttgggcc 360
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<210> 45

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 45

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<210> 46

<211> 2001

<212> DNA

<213> Homo sapiens

<400> 46

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ggtgccaatg gtgcccagcc c

2001

<210> 47

<211> 1392

<212> DNA

<213> Homo sapiens

<400> 47

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<211> 1410

<212> DNA

<213> Homo sapiens

<400> 48

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<210> 49

<211> 729

<212> DNA

<213> Homo sapiens

<400> 49

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 aaataccaag gtgtctccca ctttgaatgg acccagctcc ttgggcccggt cctgctgtca 240
 gttgggggtga cattcactct gattgctgtg tgcaagtcca aaatgctctc ctgccagttg 300
 tgcaaagaaa gtgaggaaag ggtcccggac tcggaacaga caccaggagg accatcattt 360
 gttttcactg gcatcaacca acccatcacc ttccatgggg ccaactgtggt gcagtacatc 420
 cctcctcctt atggttctcc agagcctatg gggataaata ccagctacct gcagtctgtg 480

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gtgagcccct gcggcctcat aacctctgga ggggcagcag ccgccatgtc aagtcctcct 540
 caatactaca ccatctaccc tcaagataac tctgcatttg tggttgatga gggctgcctt 600
 tctttcacgg acgggtgaaa tcacaggccc aatcctgatg ttgaccagct agaagagaca 660
 cagctggaag aggaggcctg tgccctgctt tctcctcccc cttatgaaga aatatactct 720
 ctcctcgc 729

<210> 50

<211> 810

<212> DNA

<213> Homo sapiens

<400> 50

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 tgttgccgct ggggcgcgca gcacgccggg gcccgcgagc tggctgcgct ctactcgcca 120
 ggcaagcgcc tccaggagtg gtgctctgtg atcctgtgct tcagcctcat cggccacaac 180
 ctggtccatc tcctgtgctg ggcccgttgg gaggacacac ccctcgtcat actcgggtgtt 240
 gttgcagggg ctctcattgc tgacttcttg tctggcctgg tacactgggg tgctgacaca 300
 tggggctctg tggagctgcc cattgtgggg aaggctttca tccgaccctt ccgggagcac 360
 cacattgacc caacagctat cacacggcac gacttcacg agaccaacgg ggacaactgc 420
 ctggtgacac tgctgcgct gctaaacatg gcctacaagt tccgcacca cagccctgaa 480
 gccctggagc agctataccc ctgggagtgc ttcgtcttct gcctgatcat cttcggcacc 540
 ttcaccaacc agatccacaa gtggtcgcac acgtactttg ggctgccacg ctgggtcacc 600
 ctctgcagg actggcatgt catcctgcca cgtaaacc atcgcacca ccacgtctca 660
 ccccacgaga cctacttctg catcaccaca ggctggctca actaccctct ggagaagata 720
 ggcttctggc gacgcctgga ggacctcgc cagggcctga cgggcgagaa gcctcgggca 780
 gatgacatga aatgggcccc gaagatcaaa 810

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<210> 51

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98)... (1231)

<400> 51

caagggaac gtggtttcc ctgcagagcc ggtgtctccg cctgcgtccc tgcgcagca	60
accggagctg gagtcggatc ccgaacgcac cctcgcc atg gac tcg gcc ctc agc	115
Met Asp Ser Ala Leu Ser	
1 5	
gat ccg cat aac ggc agt gcc gag gca ggc ggc ccc acc aac agc act	163
Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly Pro Thr Asn Ser Thr	
10 15 20	
acg cgg ccg cct tcc acg ccc gag ggc atc gcg ctg gcc tac ggc agc	211
Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala Leu Ala Tyr Gly Ser	
25 30 35	
ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc ggc gcc ctg cgc tcc	259
Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe Gly Ala Leu Arg Ser	
40 45 50	
gta cgc tgc gcc cgc ggc aag aat gct tca gac atg cct gaa aca atc	307
Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp Met Pro Glu Thr Ile	
55 60 65 70	

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acc agc cgg gat gcc gcc cgc ttc ccc atc atc gcc agc tgc aca ctc	355
Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile Ala Ser Cys Thr Leu	
75 80 85	
ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc cag gag tac atc aac	403
Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser Gln Glu Tyr Ile Asn	
90 95 100	
ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga atc ctg gcc ctg tcc	451
Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly Ile Leu Ala Leu Ser	
105 110 115	
cac acc atc agc ccc ttc atg aat aag ttt ttt cca gcc agc ttt cca	499
His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe Pro Ala Ser Phe Pro	
120 125 130	
aat cga cag tac cag ctg ctc ttc aca cag ggt tct ggg gaa aac aag	547
Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly Ser Gly Glu Asn Lys	
135 140 145 150	
gaa gag atc atc aat tat gaa ttt gac acc aag gac ctg gtg tgc ctg	595
Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys Asp Leu Val Cys Leu	
155 160 165	
ggc ctg agc agc atc gtt ggc gtc tgg tac ctg ctg agg aag cac tgg	643
Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu Leu Arg Lys His Trp	
170 175 180	
att gcc aac aac ctt ttt ggc ctg gcc ttc tcc ctt aat gga gta gag	691
Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe Ser Leu Asn Gly Val Glu	
185 190 195	
ctc ctg cac ctc aac aat gtc agc act ggc tgc atc ctg ctg ggc gga	739

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Leu Leu His Leu Asn Asn Val Ser Thr Gly Cys Ile Leu Leu Gly Gly
 200 205 210
 ctc ttc atc tac gat gtc ttc tgg gta ttt ggc acc aat gtg atg gtg 787
 Leu Phe Ile Tyr Asp Val Phe Trp Val Phe Gly Thr Asn Val Met Val
 215 220 225 230
 aca gtg gcc aag tcc ttc gag gca cca ata aaa ttg gtg ttt ccc cag 835
 Thr Val Ala Lys Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln
 235 240 245
 gat ctg ctg gag aaa ggc ctc gaa gca aac aac ttt gcc atg ctg gga 883
 Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly
 250 255 260
 ctt gga gat gtc gtc att cca ggg atc ttc att gcc ttg ctg ctg cgc 931
 Leu Gly Asp Val Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg
 265 270 275
 ttt gac atc agc ttg aag aag aat acc cac acc tac ttc tac acc agc 979
 Phe Asp Ile Ser Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser
 280 285 290
 ttt gca gcc tac atc ttc ggc ctg ggc ctt acc atc ttc atc atg cac 1027
 Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His
 295 300 305 310
 atc ttc aag cat gct cag cct gcc ctc cta tac ctg gtc ccc gcc tgc 1075
 Ile Phe Lys His Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys
 315 320 325
 atc ggt ttt cct gtc ctg gtg gcg ctg gcc aag gga gaa gtg aca gag 1123
 Ile Gly Phe Pro Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu

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330	335	340	
atg ttc agt tat gag gag tca aat cct aag gat cca gcg gca gtg aca			1171
Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr			
345	350	355	
gaa tcc aaa gag gga aca gag gca tca gca tcg aag ggg ctg gag aag			1219
Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys			
360	365	370	
aaa gag aaa tg atgcagctgg tgcccagagcc tctcagggcc agaccagaca			1270
Lys Glu Lys			
375			
gatgggggct gggccacac aggcgtgcac cggtagaggg cacaggaggc caagggcagc			1330
tccaggacag ggcagggggc agcaggatac ctccagccag gcctctgtgg cctctgtttc			1390
cttctccctt tcttgccct cctctgtctc tccccacacc ctgcaggcaa aagaaacccc			1450
cagcttcccc cctccccggg agccaggtgg gaaaagtggg tgtgattttt agattttgta			1510
ttgtggactg attttgctc acattaaaaa ctcacccat g			1551

<210> 52

<211> 1713

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)... (334)

<400> 52

tctcagcgcg ctgcccggct ggggacccgc gcacctgcag cgcccgtgc tcggccctgc	60
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atcctgcctg ggcatacctgc gcccggcc atg acg gcg cac tca ttc gcc etc	112
Met Thr Ala His Ser Phe Ala Leu	
1 5	
ccg gtc atc atc ttc acc acg ttc tgg ggc etc gtc ggc atc gcc ggg	160
Pro Val Ile Ile Phe Thr Thr Phe Trp Gly Leu Val Gly Ile Ala Gly	
10 15 20	
ccc tgg ttc gtg ccg aag gga ccc aac cgc gga gtg atc atc acc atg	208
Pro Trp Phe Val Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met	
25 30 35 40	
ctg gtc gcc acc gcc gtc tgc tgt tac etc ttc tgg etc atc gcc atc	256
Leu Val Ala Thr Ala Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile	
45 50 55	
ctg gcg cag ctg aac ccc ctg ttc ggg ccc cag ctg aag aat gag acc	304
Leu Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr	
60 65 70	
atc tgg tac gtg cgc ttc ctg tgg gag tgaccgcc gcccccgacc	350
Ile Trp Tyr Val Arg Phe Leu Trp Glu	
75 80	
caggtgccca gctctcgga tgactgtggc tccactgtcc ctgacaaccc cttcgtccgg	410
accctccccc acacaactat gtctgggtcac cagctccctc ctgctggcac ccagagaccc	470
ggaccgcag ggcctgcctg gttcctggaa gtcttcccag tcttcccagc cagcccgggc	530
cctgggggagc cctgggcaca gcagcggccg aggggatgtc ctgctccaat acccgcaactg	590
ctctggagtt tgccctcttt cccaaggaga tgctgctggg gagctggtat gggtggggtc	650
tttcccttta cagacggggc agatgccagg actcagccca tctgaggag gacacgtgtc	710
ctcatggaga gggtgctccg gcccaggcgg gggagtcagt gcccagtcag cagctctgcc	770

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accatcctgc tgggaactgg gggggcctct attgggttat aggcaaggcc ttttctctgg      830
catggaattg ttaattttct gacacgtcta gatgtgaaat ttctgaaaat gttgaagcag      890
agaacattc acacacaaaa agcaacatag tcatgtgggt ccagatggcc tcagtcctag      950
atgttggcac cctttgctgt gtctcctcag agtatcctgt tccgcctcct gccacctgga     1010
cctccctcag tggatgtctt ccctcccccg accccagcct gtcagtcgga gcacagtga      1070
ggtttggctc tgacttgggc ttttggctgc agtgggggtg gatttcagag cctctcatgg     1130
cagcatctaa gtgaccagag ctgggatgag agaggggaag gggcaatgtg agtggcgcta     1190
tgggacgggc cagccctgct cctgagccag ccccgccctc tgccccctgg ccctgggctc     1250
tgtgctaggg atggtgaaga atgggggcgt gccagcctgg caggagtggg aagcaacacg     1310
caggggtccc ggacctctcc agccttggcc tcacgcttac ccgagctccc agtgtggtta     1370
gcacagagct caccacactt gcctggctcc cagctggggc ctgtcctcac tggtgctcca     1430
ggggaagaaa cgacagcctc acttctgtat ggactgctga tgtggcctgc catcctgttc     1490
agcgggcatt gtctttggag cagcaggaga ataggatgcc tctactcac atgccagttc     1550
ctggctggcc agctgctcag ggctcaggct ggggcctccc attgacatcc tccccctaca     1610
ctccctctct gagcctccgt cggccctcct gttgggtaag ggtgttgagt gtgacttgtg     1670
ctgaaaacct ggttcatata taataaataa tggatgatga aag                          1713

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<210> 53

<211> 1758

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (190)... (1653)

<400> 53

105/307

tttctagggt tggaccgtgc aggcacgggc ggtcagctgg gccgcagctc ctccggctct	60
gcagggtcac ggaggaagcc agctccccta gtccaggccg agcttgcaact tgcgtcttgt	120
ctgctgctgc tgaaccaaga tttagctgtg cgccctcctt gcagtctcct ggaaccagca	180
ggaggaaac atg ggg gat act ggc ctg aga aag cgg aga gag gat gag	228
Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu	
1 5 10	
aag tcg atc cag agc caa gag cct aag acc acc agt ctc caa aag gag	276
Lys Ser Ile Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu	
15 20 25	
ctg ggc ctc atc agt ggc atc tcc atc atc gtg ggc acc atc att ggc	324
Leu Gly Leu Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly	
30 35 40 45	
tct ggg atc ttc gtt tcc ccc aag tct gtg ctc agc aac acg gaa gct	372
Ser Gly Ile Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala	
50 55 60	
gtg ggg ccc tgc ctc atc ata tgg gcg gct tgc ggg gtc ctc gcg acg	420
Val Gly Pro Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr	
65 70 75	
ctg ggt gcc ctg tgc ttt gcg gag ctt ggc aca atg atc acc aag tca	468
Leu Gly Ala Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser	
80 85 90	
ggg gga gag tat ccc tac ctg atg gag gcc tac ggg ccc atc ccc gcc	516
Gly Gly Glu Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala	
95 100 105	
tac ctc ttc tcc tgg gcc agc ctg atc gtc att aag ccc acg tcc ttc	564

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Tyr	Leu	Phe	Ser	Trp	Ala	Ser	Leu	Ile	Val	Ile	Lys	Pro	Thr	Ser	Phe		
110						115					120				125		
gcc	atc	atc	tgc	ctc	agc	ttc	tcc	gag	tat	gtg	tgt	gcg	ccc	ttc	tat	612	
Ala	Ile	Ile	Cys	Leu	Ser	Phe	Ser	Glu	Tyr	Val	Cys	Ala	Pro	Phe	Tyr		
						130					135				140		
gtg	ggc	tgc	aag	cct	cct	caa	atc	gtt	gtg	aaa	tgc	ctg	gcc	gcc	gcc	660	
Val	Gly	Cys	Lys	Pro	Pro	Gln	Ile	Val	Val	Lys	Cys	Leu	Ala	Ala	Ala		
						145					150				155		
gcc	atc	ttg	ttc	atc	tgc	aca	gtg	aac	tca	ctg	agc	gtg	cgg	ctg	gga	708	
Ala	Ile	Leu	Phe	Ile	Ser	Thr	Val	Asn	Ser	Leu	Ser	Val	Arg	Leu	Gly		
						160					165				170		
agc	tac	gtc	cag	aac	atc	ttc	acc	gcg	gcc	aag	ctg	gtg	atc	gtg	gcc	756	
Ser	Tyr	Val	Gln	Asn	Ile	Phe	Thr	Ala	Ala	Lys	Leu	Val	Ile	Val	Ala		
						175					180				185		
atc	atc	atc	atc	agc	ggg	ctg	gtg	ctc	ctg	gcc	caa	gga	aac	aca	aag	804	
Ile	Ile	Ile	Ile	Ser	Gly	Leu	Val	Leu	Leu	Ala	Gln	Gly	Asn	Thr	Lys		
190						195					200				205		
aat	ttt	gat	aat	tct	ttc	gag	ggc	gcc	cag	ctg	tct	gtg	gga	gcc	atc	852	
Asn	Phe	Asp	Asn	Ser	Phe	Glu	Gly	Ala	Gln	Leu	Ser	Val	Gly	Ala	Ile		
						210					215				220		
agc	ctg	gcg	ttt	tac	aat	gga	ctc	tgg	gcc	tat	gat	gga	tgg	aat	caa	900	
Ser	Leu	Ala	Phe	Tyr	Asn	Gly	Leu	Trp	Ala	Tyr	Asp	Gly	Trp	Asn	Gln		
						225					230				235		
ctc	aat	tac	atc	aca	gaa	gaa	ctt	aga	aac	cct	tac	aga	aac	ctg	cct	948	
Leu	Asn	Tyr	Ile	Thr	Glu	Glu	Leu	Arg	Asn	Pro	Tyr	Arg	Asn	Leu	Pro		

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240	245	250	
ttg gcc att atc atc ggg atc ccc ctg gtg acg gcg tgc tac atc ctc			996
Leu Ala Ile Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu			
255	260	265	
atg aac gtg tcc tac ttc acc gtg atg act gcc acc gaa ctc ctg cag			1044
Met Asn Val Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln			
270	275	280	285
tcc cag gcg gtg gct gtg aca ttt ggt gac cgt gtt ctc tat cct gct			1092
Ser Gln Ala Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala			
	290	295	300
tct tgg atc gtt cca ctt ttt gtg gca ttt tca acc atc ggt gct gct			1140
Ser Trp Ile Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala			
	305	310	315
aac ggg acc tgc ttc aca gcg ggc aga ctc att tac gtg gcg ggc cgg			1188
Asn Gly Thr Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg			
	320	325	330
gag ggt cac atg ctc aaa gtg ctt tct tac atc agc gtc agg cgc ctc			1236
Glu Gly His Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu			
	335	340	345
act cca gcc ccc gcc atc atc ttt tat ggt atc ata gca acg att tat			1284
Thr Pro Ala Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr			
350	355	360	365
atc atc cct ggt gac ata aac tcg tta gtc aat tat ttc agc ttt gcc			1332
Ile Ile Pro Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala			
	370	375	380

108/307

gca tgg ctg ttt tat ggc ctg acg att cta gga ctc atc gtg atg aga 1380
 Ala Trp Leu Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg
 385 390 395
 ttt aca agg aaa gag ctg gaa agg cct atc aag gtg ccc gta gtc att 1428
 Phe Thr Arg Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile
 400 405 410
 ccc gtc ttg atg aca ctc atc tct gtg ttt ttg gtt ctg gct cca atc 1476
 Pro Val Leu Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile
 415 420 425
 atc agc aag ccc acc tgg gag tac ctc tac tgt gtg ctg ttt ata tta 1524
 Ile Ser Lys Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu
 430 435 440 445
 agc ggc ctt tta ttt tac ttc ctg ttt gtc cac tac aag ttt gga tgg 1572
 Ser Gly Leu Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp
 450 455 460
 gct cag aaa atc tca aag ccg att acc atg cac ctt cag atg cta atg 1620
 Ala Gln Lys Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met
 465 470 475
 gaa gtg gtc cca ccg gag gaa gac cct gag taacaagctc cgtctcttgt 1670
 Glu Val Val Pro Pro Glu Glu Asp Pro Glu
 480 485
 agccaagtca gctgaattta ttttcttaag caatatttgt gggtatttct tccttttttt 1730
 cttacgaata aaatatactc agatgttt 1758

109/307

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (154)... (1281)

<400> 54

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gggcctccgc ccgcctggga agcagagaga aagccgggcc cagcccttcc tcacccttcc	120
cctccccgca ccgcccggag aggtcggacg gcg atg acc ccc cag ccc gcc gga	174
Met Thr Pro Gln Pro Ala Gly	
1 5	
ccc ccg gat ggg ggc tgg ggc tgg gtg gtg gcg gcc gca gcc ttc gcg	222
Pro Pro Asp Gly Gly Trp Gly Trp Val Val Ala Ala Ala Ala Phe Ala	
10 15 20	
ata aac ggg ctg tcc tac ggg ctg ctg cgc tcg ctg ggc ctt gcc ttc	270
Ile Asn Gly Leu Ser Tyr Gly Leu Leu Arg Ser Leu Gly Leu Ala Phe	
25 30 35	
cct gac ctt gcc gag cac ttt gac cga agc gcc cag gac act gcg tgg	318
Pro Asp Leu Ala Glu His Phe Asp Arg Ser Ala Gln Asp Thr Ala Trp	
40 45 50 55	
atc agc gcc ctg gcc ctg gcc gtg cag cag gca gcc agc ccc gtg ggc	366
Ile Ser Ala Leu Ala Leu Ala Val Gln Gln Ala Ala Ser Pro Val Gly	
60 65 70	
agc gcc ctg agc acg cgc tgg ggg gcc cgc ccc gtg gtg atg gtt ggg	414

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Ser Ala Leu Ser Thr Arg Trp Gly Ala Arg Pro Val Val Met Val Gly
 75 80 85
 ggc gtc ctc gcc tcg ctg ggc ttc gtc ttc tcg gct ttc gcc agc ggt 462
 Gly Val Leu Ala Ser Leu Gly Phe Val Phe Ser Ala Phe Ala Ser Gly
 90 95 100
 ctg ctg cat ctc tac ctc ggc ctg ggc ctc ctc gct ggc ttt ggt tgg 510
 Leu Leu His Leu Tyr Leu Gly Leu Gly Leu Leu Ala Gly Phe Gly Trp
 105 110 115
 gcc ctg gtg ttc gcc ccc gcc cta ggc acc ctc tcg cgt tac ttc tcc 558
 Ala Leu Val Phe Ala Pro Ala Leu Gly Thr Leu Ser Arg Tyr Phe Ser
 120 125 130 135
 cgc cgt cga gtc ttg gcg gtg ggg ctg gcg ctc acc ggc aac ggg gcc 606
 Arg Arg Arg Val Leu Ala Val Gly Leu Ala Leu Thr Gly Asn Gly Ala
 140 145 150
 tcc tcg ctg ctc ctg gcg ccc gcc ttg cag ctt ctc ctc gat act ttc 654
 Ser Ser Leu Leu Leu Ala Pro Ala Leu Gln Leu Leu Leu Asp Thr Phe
 155 160 165
 ggc tgg cgg ggc gct ctg ctc ctc ctc ggc gcg atc acc ctc cac ctc 702
 Gly Trp Arg Gly Ala Leu Leu Leu Leu Gly Ala Ile Thr Leu His Leu
 170 175 180
 acc ccc tgt ggc gcc ctg ctg cta ccc ctg gtc ctt cct gga gac ccc 750
 Thr Pro Cys Gly Ala Leu Leu Leu Pro Leu Val Leu Pro Gly Asp Pro
 185 190 195
 cca gcc cca ccg cgt agt ccc cta gct gcc ctc ggc ctg agt ctg ttc 798
 Pro Ala Pro Pro Arg Ser Pro Leu Ala Ala Leu Gly Leu Ser Leu Phe

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200	205	210	215	
aca cgc cgg gcc ttc tca atc ttt gct cta ggc aca gcc ctg gtt ggg				846
Thr Arg Arg Ala Phe Ser Ile Phe Ala Leu Gly Thr Ala Leu Val Gly				
220	225	230		
ggc ggg tac ttc gtt cct tac gtg cac ttg gct ccc cgc ttt aga ccg				894
Gly Gly Tyr Phe Val Pro Tyr Val His Leu Ala Pro Arg Phe Arg Pro				
235	240	245		
ggg cct ggg ggg ata cgg agc agc gct ggt ggt ggc cgt ggc tgc gat				942
Gly Pro Gly Gly Ile Arg Ser Ser Ala Gly Gly Gly Arg Gly Cys Asp				
250	255	260		
ggg gga tgc ggg cgc ccg gct ggt ctg cgg gtg gct ggc aga cca agg				990
Gly Gly Cys Gly Arg Pro Ala Gly Leu Arg Val Ala Gly Arg Pro Arg				
265	270	275		
ctg ggt gcc cct ccc gcg gct gct ggc cgt att cgg ggc tct gac tgg				1038
Leu Gly Ala Pro Pro Ala Ala Ala Gly Arg Ile Arg Gly Ser Asp Trp				
280	285	290	295	
gct ggg gct gtg ggt ggt ggg gct ggt gcc cgt ggt ggg cgg cga aga				1086
Ala Gly Ala Val Gly Gly Gly Ala Gly Ala Arg Gly Gly Arg Arg Arg				
300	305	310		
gag ctg ggg ggg tcc cct gct ggc cgc ggc tgt ggc cta tgg gct gag				1134
Glu Leu Gly Gly Ser Pro Ala Gly Arg Gly Cys Gly Leu Trp Ala Glu				
315	320	325		
cgc ggg gag tta cgc ccc gct ggt ttt cgg tgt act ccc cgg gct ggt				1182
Arg Gly Glu Leu Arg Pro Ala Gly Phe Arg Cys Thr Pro Arg Ala Gly				
330	335	340		

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ggg cgt cgg agg tgt ggt gca ggc cac agg gct ggt gat gat gct gat 1230

Gly Arg Arg Arg Cys Gly Ala Gly His Arg Ala Gly Asp Asp Ala Asp

345

350

355

gag cct cgg ggg gct cct ggg ccc tcc cct gtc agg ctt cct aag gga 1278

Glu Pro Arg Gly Ala Pro Gly Pro Ser Pro Val Arg Leu Pro Lys Gly

360

365

370

375

tg agacaggaga cttcaccgcc tctttctctc tgtctggttc ttgatactc 1330

tccggcagct tcattacat agggttgcc agggcgctgc cctcctgtgg tccagcctcc 1390

cctccagcca cgcctcccc agagacgggg gagctgcttc ccgctcccca ggcagtcttg 1450

ctgtccccag gaggcctgg ctccactctg gacaccactt gttgattatt ttcttgtttg 1510

agccccctccc ccaataaaga atttttatcg ggttttcctg 1550

<210> 55

<211> 1485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)... (1153)

<400> 55

ctctcctcga ccctggacgt ctaccttcg gaggccaca tcttgccac tccgcgcgcg 60

gggctagcgc gggtttcagc gacgggagcc ctcaaggac atg gca act aca gcg 115

Met Ala Thr Thr Ala

1

5

gcg ccg gcg ggc ggc gcc cga aat gga gct ggc ccg gaa tgg gga ggg 163

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Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly Pro Glu Trp Gly Gly	
10 15 20	
ttc gaa gaa aac atc cag ggc gga ggc tca gct gtg att gac atg gag	211
Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala Val Ile Asp Met Glu	
25 30 35	
aac atg gat gat acc tca ggc tct agc ttc gag gat atg ggt gag ctg	259
Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu Asp Met Gly Glu Leu	
40 45 50	
cat cag cgc ctg cgc gag gaa gaa gta gac gct gat gca gct gat gca	307
His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala Asp Ala Ala Asp Ala	
55 60 65	
gct gct gct gaa gag gag gat gga gag ttc ctg ggc atg aag ggc ttt	355
Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu Gly Met Lys Gly Phe	
70 75 80 85	
aag gga cag ctg agc cgg cag gtg gca gat cag atg tgg cag gct ggg	403
Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln Met Trp Gln Ala Gly	
90 95 100	
aaa aga caa gcc tcc agg gcc ttc agc ttg tac gcc aac atc gac atc	451
Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr Ala Asn Ile Asp Ile	
105 110 115	
ctc aga ccc tac ttt gat gtg gag cct gct cag gtg cga agc agg ctc	499
Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln Val Arg Ser Arg Leu	
120 125 130	
ctg gag tcc atg atc cct atc aag atg gtc aac ttc ccc cag aaa att	547
Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn Phe Pro Gln Lys Ile	

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135	140	145	
gca ggt gaa ctc tat gga cct ctc atg ctg gtc ttc act ctg gtt gct			595
Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala			
150	155	160	165
atc cta ctc cat ggg atg aag acg tct gac act att atc cgg gag ggc			643
Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly			
	170	175	180
acc ctg atg ggc aca gcc att ggc acc tgc ttc ggc tac tgg ctg gga			691
Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly			
	185	190	195
gtc tca tcc ttc att tac ttc ctt gcc tac ctg tgc aac gcc cag atc			739
Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile			
200	205	210	
acc atg ctg cag atg ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat			787
Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His			
215	220	225	
tgc att gtc ctg ttc atc acc tat aat atc cac ctc cac gcc ctc ttc			835
Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His Leu His Ala Leu Phe			
230	235	240	245
tac ctc ttc tgg ctg ttg gtg ggt gga ctg tcc aca ctg cgc atg gta			883
Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val			
	250	255	260
gca gtg ttg gtg tct cgg acc gtg ggc ccc aca cag cgg ctg ctc ctc			931
Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr Gln Arg Leu Leu Leu			
265	270	275	

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tgt ggc acc ctg gct gcc cta cac atg ctc ttc ctg ctc tat ctg cat 979
 Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe Leu Leu Tyr Leu His
 280 285 290
 ttt gcc tac cac aaa gtg gta gag ggg atc ctg gac aca ctg gag ggc 1027
 Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu Asp Thr Leu Glu Gly
 295 300 305
 ccc aac atc ccg ccc atc cag agg gtc ccc aga gac atc cct gcc atg 1075
 Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met
 310 315 320 325
 ctc cct gct gct cgg ctt ccc acc acc gtc ctc aac gcc aca gcc aaa 1123
 Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys
 330 335 340
 gct gtt gcg gtg acc ctg cag tca cac tgacccacc tgaaattctt 1170
 Ala Val Ala Val Thr Leu Gln Ser His
 345 350
 ggccagtctt ctttcccgca gctgcagaga ggaggaagac tattaaagga cagtcctgat 1230
 gacatgtttc gtagatgggg ttgacagctg ccactgagct gtagctgcgt aagtacctcc 1290
 ttgatgcctg tcggcacttc tgaaaggcac aaggccaaga actcctggcc aggactgcaa 1350
 ggctctgcag ccaatgcaga aaatgggtca gtcctttga gaaccctcc ccacctacc 1410
 cttccttctt ctttatctct cccacattgt cttgctaaat atagacttgg taattaaaat 1470
 gttgattgaa gtctg 1485

<210> 56

<211> 2694

<212> DNA

116/307

<213> Homo sapiens

<220>

<221> CDS

<222> (80)... (2083)

<400> 56

gtagactctg cggtatcccg gaccagcgcc actcatcctg cagcactggg gacagacaga	60
gcaggagaag ggccagaga atg tcg tcc cag cca gca ggg aac cag acc tcc	112
Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser	
1 5 10	
ccc ggg gcc aca gag gac tac tcc tat ggc agc tgg tac atc gat gag	160
Pro Gly Ala Thr Glu Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu	
15 20 25	
ccc cag ggg ggc gag gag ctc cag cca gag ggg gaa gtg ccc tcc tgc	208
Pro Gln Gly Gly Glu Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys	
30 35 40	
cac acc agc ata cca ccc ggc ctg tac cac gcc tgc ctg gcc tcg ctg	256
His Thr Ser Ile Pro Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu	
45 50 55	
tca atc ctt gtg ctg ctg ctc ctg gcc atg ctg gtg agg cgc cgc cag	304
Ser Ile Leu Val Leu Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln	
60 65 70 75	
ctc tgg cct gac tgt gtg cgt ggc agg ccc ggc ctg ccc agc cct gtg	352
Leu Trp Pro Asp Cys Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val	
80 85 90	
gat ttc ttg gct ggg gac agg ccc cgg gca gtg cct gct gct gtt ttc	400

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Asp Phe Leu Ala Gly Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe
 95 100 105
 atg gtc ctc ttg agc tcc ctg tgt ttg ctg ctc ccc gac gag gac gca 448
 Met Val Leu Leu Ser Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala
 110 115 120
 ttg ccc ttc ctg act ctc gcc tca gca ccc agc caa gat ggg aaa act 496
 Leu Pro Phe Leu Thr Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr
 125 130 135
 gag gct cca aga ggg gcc tgg aag ata ctg gga ctg ttc tat tat gct 544
 Glu Ala Pro Arg Gly Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala
 140 145 150 155
 gcc ctc tac tac cct ctg gct gcc tgt gcc acg gct ggc cac aca gct 592
 Ala Leu Tyr Tyr Pro Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala
 160 165 170
 gca cac ctg ctc ggc agc acg ctg tcc tgg gcc cac ctt ggg gtc cag 640
 Ala His Leu Leu Gly Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln
 175 180 185
 gtc tgg cag agg gca gag tgt ccc cag gtg ccc aag atc tac aag tac 688
 Val Trp Gln Arg Ala Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr
 190 195 200
 tac tcc ctg ctg gcc tcc ctg cct ctc ctg ctg ggc ctc gga ttc ctg 736
 Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu
 205 210 215
 agc ctt tgg tac cct gtg cag ctg gtg aga agc ttc agc cgt agg aca 784
 Ser Leu Trp Tyr Pro Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr

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220	225	230	235	
gga gca ggc tcc aag ggg ctg cag agc agc tac tct gag gaa tat ctg				832
Gly Ala Gly Ser Lys Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu				
	240	245	250	
agg aac ctc ctt tgc agg aag aag ctg gga agc agc tac cac acc tcc				880
Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser				
	255	260	265	
aag cat ggc ttc ctg tcc tgg gcc cgc gtc tgc ttg aga cac tgc atc				928
Lys His Gly Phe Leu Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile				
	270	275	280	
tac act cca cag cca gga ttc cat ctc ccg ctg aag ctg gtg ctt tca				976
Tyr Thr Pro Gln Pro Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser				
	285	290	295	
gct aca ctg aca ggg acg gcc att tac cag gtg gcc ctg ctg ctg ctg				1024
Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu				
300	305	310	315	
gtg ggc gtg gta ccc act atc cag aag gtg agg gca ggg gtc acc acg				1072
Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr				
	320	325	330	
gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc tcc gag gac				1120
Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp				
	335	340	345	
aag cag gag gtg gtg gag ctg gtg aag cac cat ctg tgg gct ctg gaa				1168
Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp Ala Leu Glu				
	350	355	360	

119/307

gtg tgc tac atc tca gcc ttg gtc ttg tcc tgc tta ctc acc ttc ctg	1216
Val Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu	
365 370 375	
gtc ctg atg cgc tca ctg gtg aca cac agg acc aac ctt cga gct ctg	1264
Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu	
380 385 390 395	
cac cga gga gct gcc ctg gac ttg agt ccc ttg cat cgg agt ccc cat	1312
His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser Pro His	
400 405 410	
ccc tcc cgc caa gcc ata ttc tgt tgg atg agc ttc agt gcc tac cag	1360
Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln	
415 420 425	
aca gcc ttt atc tgc ctt ggg ctc ctg gtg cag cag atc atc ttc ttc	1408
Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe	
430 435 440	
ctg gga acc acg gcc ctg gcc ttc ctg gtg ctc atg cct gtg ctc cat	1456
Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val Leu His	
445 450 455	
ggc agg aac ctc ctg ctc ttc cgt tcc ctg gag tcc tcg tgg ccc ttc	1504
Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe	
460 465 470 475	
tgg ctg act ttg gcc ctg gct gtg atc ctg cag aac atg gca gcc cat	1552
Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala Ala His	
480 485 490	
tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg acc aac cgg	1600

120/307

Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg
 495 500 505
 cga gtg ctc tat gca gcc acc ttt ctt ctc ttc ccc ctc aat gtg ctg 1648
 Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu
 510 515 520
 gtg ggt gcc atg gtg gcc acc tgg cga gtg ctc ctc tct gcc ctc tac 1696
 Val Gly Ala Met Val Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr
 525 530 535
 aac gcc atc cac ctt ggc cag atg gac ctc agc ctg ctg cca ccg aga 1744
 Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg
 540 545 550 555
 gcc gcc act ctc gac ccc ggc tac tac acg tac cga aac ttc ttg aag 1792
 Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys
 560 565 570
 att gaa gtc agc cag tcg cat cca gcc atg aca gcc ttc tgc tcc ctg 1840
 Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu
 575 580 585
 ctc ctg caa gcg cag agc ctc cta ccc agg acc atg gca gcc ccc cag 1888
 Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln
 590 595 600
 gac agc ctc aga cca ggg gag gaa gac gaa ggg atg cag ctg cta cag 1936
 Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln
 605 610 615
 aca aag gac tcc atg gcc aag gga gct agg ccc ggg gcc agc cgc ggc 1984
 Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly

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620	625	630	635	
agg gct cgc tgg ggt ctg gcc tac acg ctg ctg cac aac cca acc ctg				2032
Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu				
	640	645	650	
cag gtc ttc cgc aag acg gcc ctg ttg ggt gcc aat ggt gcc cag ccc				2080
Gln Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro				
	655	660	665	
tgagggcagg gaaggtcaac ccacctgccc atctgtgctg aggcatgttc				2130
ctgcctacca tcttcctccc tccccggctc tctcccagc atcacaccag ccatgcagcc				2190
agcaggtcct ccggatcacc gtggttgggt ggaggtctgt ctgcaactggg agcctcagga				2250
gggctctgct ccaccactt ggctatggga gagccagcag gggttctgga gaaagaaact				2310
ggtggggttag ggccttggtc caggagccag ttgagccagg gcagccacat ccaggcgtct				2370
ccctaccctg gctctgccat cagccttgaa gggcctcgat gaagccttct ctggaaccac				2430
tccagcccag ctccacctca gccttggcct tcacgtgtg gaagcagcca aggcacttcc				2490
tcacccctc agcgccacgg acctctctgg ggagtggccg gaaagctccc gggcctctgg				2550
cctgcagggc agcccaagtc atgactcaga ccaggtecca cactgagctg cccacactcg				2610
agagccagat atttttgtag tttttatgcc tttggctatt atgaaagagg ttagtgtgtt				2670
ccctgcaata aacttggtcc tgag				2694

<210> 57

<211> 3297

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

122/307

<222> (83)... (1477)

<400> 57

ggggtctgta ctctgtgaag tcaactgggt tagtgtgctc tctgatgcct ggaattccag	60
tccccaccca gaaaccgca gc atg att gtc tgc ctc ctt ttc atg atg att	112
Met Ile Val Cys Leu Leu Phe Met Met Ile	
1 5 10	
tta ttg gca aag gaa gtt caa ctg gta gac caa aca gat tca cct tta	160
Leu Leu Ala Lys Glu Val Gln Leu Val Asp Gln Thr Asp Ser Pro Leu	
15 20 25	
ctt agt ctc ctt gga cag aca agc tca ctt tca tgg cat ctt gtg gat	208
Leu Ser Leu Leu Gly Gln Thr Ser Ser Leu Ser Trp His Leu Val Asp	
30 35 40	
att gtg tgc tac cag agt gtg cta agt tat ttc agc agc cat tac ccg	256
Ile Val Ser Tyr Gln Ser Val Leu Ser Tyr Phe Ser Ser His Tyr Pro	
45 50 55	
ccg tcc atc atc ctg gca aaa gaa tct tat gct gaa tta atc atg aag	304
Pro Ser Ile Ile Leu Ala Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys	
60 65 70	
ctc cta aaa gtg tct gcg ggc ctt tct att cct act gac agc cag aag	352
Leu Leu Lys Val Ser Ala Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys	
75 80 85 90	
cat ctt gat gca gtt cca aaa tgc caa gct ttt act cat cag atg gtt	400
His Leu Asp Ala Val Pro Lys Cys Gln Ala Phe Thr His Gln Met Val	
95 100 105	
caa ttc ctc agc acc ctg gaa caa aat gga aaa atc acc tta gca gtc	448

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Gln Phe Leu Ser Thr Leu Glu Gln Asn Gly Lys Ile Thr Leu Ala Val
 110 115 120
 cta gaa cag gaa atg tct aag ctc tta gac gat atc att gtc ttt aac 496
 Leu Glu Gln Glu Met Ser Lys Leu Leu Asp Asp Ile Ile Val Phe Asn
 125 130 135
 ccg ccc gac atg gac agc cag acc cgc cac atg gcc ctc agc agc ctc 544
 Pro Pro Asp Met Asp Ser Gln Thr Arg His Met Ala Leu Ser Ser Leu
 140 145 150
 ttt atg gaa gtc ctg atg atg atg aac aac gcg act att cca aca gca 592
 Phe Met Glu Val Leu Met Met Met Asn Asn Ala Thr Ile Pro Thr Ala
 155 160 165 170
 gag ttc ctt cgg ggc agt atc cgg acc tgg att ggc caa aaa atg cat 640
 Glu Phe Leu Arg Gly Ser Ile Arg Thr Trp Ile Gly Gln Lys Met His
 175 180 185
 ggg ctg gtg gtg ctg ccc ctt tta aca gca gcc tgc cag agc ctg gcg 688
 Gly Leu Val Val Leu Pro Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala
 190 195 200
 tcc gtc cgc cac atg gct gag act aca gaa gcc tgc atc act gcc tac 736
 Ser Val Arg His Met Ala Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr
 205 210 215
 ttc aaa gaa agc cct ctc aat cag aat tca gga tgg gga ccc att ctg 784
 Phe Lys Glu Ser Pro Leu Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu
 220 225 230
 gta tcc ctt cag gtt ccc gag ctc acc atg gaa gag ttc ctg cag gag 832
 Val Ser Leu Gln Val Pro Glu Leu Thr Met Glu Glu Phe Leu Gln Glu

124/307

235	240	245	250	
tgc ctc acc ttg ggc agt tac ttg act ctt tac gtc tac ttg ctt cag				880
Cys Leu Thr Leu Gly Ser Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln				
	255	260	265	
tgt tta aac agc gaa cag act tta agg aat gaa atg aaa gtg ctg ctc				928
Cys Leu Asn Ser Glu Gln Thr Leu Arg Asn Glu Met Lys Val Leu Leu				
	270	275	280	
atc tta agc aag tgg ctg gaa cag gtg tac cca agc tcc gtg gag gaa				976
Ile Leu Ser Lys Trp Leu Glu Gln Val Tyr Pro Ser Ser Val Glu Glu				
	285	290	295	
gag gca aag ctg ttt ttg tgg tgg cac caa gtc ctt cag ctc tcc ctc				1024
Glu Ala Lys Leu Phe Leu Trp Trp His Gln Val Leu Gln Leu Ser Leu				
	300	305	310	
att cag aca gag cag aat gac tcc gtc ctg aca gaa tct gtc att cga				1072
Ile Gln Thr Glu Gln Asn Asp Ser Val Leu Thr Glu Ser Val Ile Arg				
	315	320	325	330
att ctg ctc ttg gtt cag agc agg cag aac ctc gtg gct gag gag aga				1120
Ile Leu Leu Leu Val Gln Ser Arg Gln Asn Leu Val Ala Glu Glu Arg				
	335	340	345	
ctc agc tct ggg atc ctg ggg gca att ggg ttt ggc cgg aag tcg cct				1168
Leu Ser Ser Gly Ile Leu Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro				
	350	355	360	
ttg tct aac agg ttc cga gtg gtt gcc cga agc atg gct gcc ttc ctt				1216
Leu Ser Asn Arg Phe Arg Val Val Ala Arg Ser Met Ala Ala Phe Leu				
	365	370	375	

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tca gtt cag gtt cct atg gaa gat cag atc cgt ttg agg cct ggc tct	1264
Ser Val Gln Val Pro Met Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser	
380 385 390	
gaa tta cat ctg acc ccc aaa gct cag cag gct ctg aat gct ctt gaa	1312
Glu Leu His Leu Thr Pro Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu	
395 400 405 410	
tcc atg gca tca agt aag cag tat gtt gaa tac cag gat caa ata ttg	1360
Ser Met Ala Ser Ser Lys Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu	
415 420 425	
caa gcc acc caa ttt ata agg cat cct ggc cat tgc ctt caa gat ggg	1408
Gln Ala Thr Gln Phe Ile Arg His Pro Gly His Cys Leu Gln Asp Gly	
430 435 440	
aaa agc ttc ttg gct ctt ctc gtt aac tgt ctg tat cca gaa gtg cat	1456
Lys Ser Phe Leu Ala Leu Leu Val Asn Cys Leu Tyr Pro Glu Val His	
445 450 455	
tat ttg gac cac ata cga tagtta aactgaggc tcttgaaaaa cccattgctg	1510
Tyr Leu Asp His Ile Arg	
460	
tttatgttta catttaactt tgctgttgca caagtaactt tgctcaattg cactgtagag	1570
ctcagtttgg ccaatgtgta gttgactgag atgcaagttg ggaggcgtta gatattagat	1630
aattttgggg tgtgtgtgtg tgtgtgtgtg tgttttctta gctcttaaga ccttctgggg	1690
actctttaag tttttatatt tatccacaag agaaacttac taagttccac ttgggtgcag	1750
agccactcac agttgccgaa tgtcccgatc atctcacaag acctccagat ggagttcttt	1810
gtatgtttcc acttctgtct ctgttttatg taaatgttcc agatctgaca accttggaag	1870
tcactcagta cccttacttt taaaccccat ttgtgttcct ccaaagtaaa gaagtcaatt	1930

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ttgaaaaatt tctgcatttc tcaaatgtgg acaaatacaa tagttttaaa gtattgtttt	1990
tctcagaagg gagataaaaa tgccgagtta gttaaagtgg gtcattgtga aaatacagacc	2050
acttgatcgt gattatagtg ggcagtagag atgatgacaa gtcaatttcc atccagccgt	2110
gtatcctcat ggagaagctg cctgtctgaa tcaggatggc aagctggcag tctgggagga	2170
gcatgttttg cacagatgtt ttgtttgtc cacttggtga ggagtgcaga cagggtgcc	2230
tctctctagt cgggagagtc tgtgcattcc ctggggccct gaccctagcc tcattcacat	2290
cacttgcccc tgtcgacacc taagtttgca ccctttgata gacacatgt tcgatatctg	2350
aaaggctcag tgtcaggaga cagagactga gggagactga agacctgatt cctgtttccc	2410
tgttgtttt ttaacttcaa actcagatga agccaatgga cctgctgaaa cacttgtctg	2470
tggaaactgg gtcaggctgg gagatctact gaaatttggc tttttttcca tagccacgtg	2530
ccttctgttg ttgacagttc attcattacc aaagcctgtg tgtaactttg cctgtttctg	2590
tggccatctt ctgtctcatg ttatttctcc tgggaatgag cagtttgact tctgttccca	2650
cgttcctcat tctatcagct ctagatggat ttgcctgca tagctggctt aatatgtctt	2710
tgtgtatggg tagtctgtag cctgagaata ttacctaata aatgtctaaa cagccaccaa	2770
gaatgtttat aggggtatag gaatatagtt aacagagtgc taatctctcc tcaaatgtcc	2830
ttttggaatg ctcccccaa aattgggaag ttggtaggag cttttcttta ctttgaattt	2890
ctttacttgg acagaacgat tctgccttaa agacacgctt tgcagctctg ataaagaaca	2950
tccctgttta gtctcttgag ttttacaggc caaaaaatgt ccgtctcaga gggatctgtc	3010
tcagcttttc ttatttttgc ttctctccgt tttcaaaatt aatcatcttg ttctctgtat	3070
aagaaaattt gagaagctgt ggacaattta atagtctgat ctggcaacag cgatttttgt	3130
ttggaaatat tttgtgtttt ctttgaggag gatataatta ctgatatcct aggatgtgaa	3190
atttttgagt gacagtatgc acatttttaa gaaaattatg attaactctgt ataattgttt	3250
ttggtctgta aaaattataa aaaataaaat catttatctt tggttgt	3297

127/307

<211> 2126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61)... (1473)

<400> 58

aacactgaca gcgtgagccc gcggcggctg ctgccatggt ggctggcggc cgggtgcagc	60
atg tct aga ctg gga gcc ctg ggt ggt gcc cgt gcc ggg ctg gga ctg	108
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu	
1 5 10 15	
ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc	156
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser	
20 25 30	
cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc	204
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro	
35 40 45	
aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg	252
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met	
50 55 60	
ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc	300
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro	
65 70 75 80	
agc ctt cca cgg gaa gga cag gag aag gtg ctg gac cgc ctg gac ttt	348
Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe	

128/307

85	90	95	
gtg ctg acc agc ctt	gtg gcg ctg cgg cgg gag	gtg gag gag ctg aga	396
Val Leu Thr Ser Leu Val	Ala Leu Arg Arg Glu Val	Glu Glu Leu Arg	
100	105	110	
agc agc ctg cga ggg ctt	gcg ggg gag att gtt	ggg gag gtc cga tgc	444
Ser Ser Leu Arg Gly Leu	Ala Gly Glu Ile Val	Gly Glu Val Arg Cys	
115	120	125	
cac atg gaa gag aac cag	aga gtg gct cgg cgg cga	agg ttt ccg ttt	492
His Met Glu Glu Asn Gln	Arg Val Ala Arg Arg Arg	Arg Phe Pro Phe	
130	135	140	
gtc cgg gag agg agt gac	tcc act ggc tcc agc tct	gtc tac ttc acg	540
Val Arg Glu Arg Ser Asp	Ser Thr Gly Ser Ser Ser	Val Tyr Phe Thr	
145	150	155	160
gcc tcc tcg gga gcc acg	ttc aca gat gct gag agt	gaa ggg ggt tac	588
Ala Ser Ser Gly Ala Thr	Phe Thr Asp Ala Glu Ser	Glu Gly Gly Tyr	
165	170	175	
aca aca gcc aat gcg gag	tct gac aat gag cgg gac	tct gac aaa gaa	636
Thr Thr Ala Asn Ala Glu	Ser Asp Asn Glu Arg Asp	Ser Asp Lys Glu	
180	185	190	
agt gag gac ggg gaa gat	gaa gtg agc tgt gag act	gtg aag atg ggg	684
Ser Glu Asp Gly Glu Asp	Glu Val Ser Cys Glu Thr	Val Lys Met Gly	
195	200	205	
aga aag gat tct ctt gac	ttg gag gaa gag gca gct	tca ggt gcc tcc	732
Arg Lys Asp Ser Leu Asp	Leu Glu Glu Glu Ala Ala	Ser Gly Ala Ser	
210	215	220	

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agt gcc ctg gag gct gga ggt tcc tca ggc ttg gag gat gtg ctg ccc	780
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro	
225 230 235 240	
ctc ctg cag cag gcc gac gag ctg cac agg ggt gat gag caa ggc aag	828
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys	
245 250 255	
cgg gag ggc ttc cag ctg ctg ctc aac aac aag ctg gtg tat gga agc	876
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser	
260 265 270	
cgg cag gac ttt ctc tgg cgc ctg gcc cga gcc tac agt gac atg tgt	924
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys	
275 280 285	
gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga	972
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly	
290 295 300	
aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac	1020
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp	
305 310 315 320	
tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag	1068
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu	
325 330 335	
agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg	1116
Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val	
340 345 350	
gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt	1164

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Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu
 355 360 365
 ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa 1212
 Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys
 370 375 380
 aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa 1260
 Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu
 385 390 395 400
 gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt 1308
 Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe
 405 410 415
 tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg 1356
 Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly
 420 425 430
 aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca 1404
 Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro
 435 440 445
 gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg 1452
 Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu
 450 455 460
 gaa gtc att tta cga gac taaccacgtt tcaactggcct tcatgacttg 1500
 Glu Val Ile Leu Arg Asp
 465 470
 atgccactat ttaaggtggg ggggcgggga ggcttttttc cttagacctt gctgagatca 1560
 ggaaaccaca caaatctgtc tcctgggtct gactgctacc cactaccact cccattagt 1620

131/307

taatttattc taacctctaa cctaattctag aattggggca gtactcatgg cttccgtttc 1680
 tgttgttctc tcccttgagt aatctcttaa aaaaatcaag attcacacct gccccaggat 1740
 tacacatggg tagagcctgc aagacctgag accttccaat tgctgggtgag gtggatgaac 1800
 ttcaaagcta taggaacaaa gcacataact tgcacttta atctttttca ctgactaata 1860
 ggactcagta catatagtct taagatcata ccttacctac caaggtaaaa agagggatca 1920
 gagtggccca cagacattgc tttcttatca cctatcatgt gaattctacc tgtattcctg 1980
 ggctggacca cttgataact tccagtgtcc tggcagcttt tggaatgaca gcagtggat 2040
 ggggtttatg atgctataaa acaatgtctg aaaagttgcc tagaatatat tttgttacia 2100
 acttgaaata aaccaaattt gatgtt 2126

<210> 59

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)... (805)

<400> 59

aatttgacc tgtgattcct tggttctcac aatcctctcc actctaagaa gcagggtgag 60
 cccacaagga gca atg gag cag ggc agc ggc cgc ttg gag gac ttc cct 109

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro

1

5

10

gtc aat gtg ttc tcc gtc act cct tac aca ccc agc acc gct gac atc 157

Val Asn Val Phe Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile

15

20

25

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cag gtg tcc gat gat gac aag gcg ggg gcc acc ttg ctc ttc tca ggc	205
Gln Val Ser Asp Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly	
30 35 40	
atc ttt ctg gga ctg gtg ggg atc aca ttc act gtc atg ggc tgg atc	253
Ile Phe Leu Gly Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile	
45 50 55 60	
aaa tac caa ggt gtc tcc cac ttt gaa tgg acc cag ctc ctt ggg ccc	301
Lys Tyr Gln Gly Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro	
65 70 75	
gtc ctg ctg tca gtt ggg gtg aca ttc atc ctg att gct gtg tgc aag	349
Val Leu Leu Ser Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys	
80 85 90	
ttc aaa atg ctc tcc tgc cag ttg tgc aaa gaa agt gag gaa agg gtc	397
Phe Lys Met Leu Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val	
95 100 105	
ccg gac tcg gaa cag aca cca gga gga cca tca ttt gtt ttc act ggc	445
Pro Asp Ser Glu Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly	
110 115 120	
atc aac caa ccc atc acc ttc cat ggg gcc act gtg gtg cag tac atc	493
Ile Asn Gln Pro Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile	
125 130 135 140	
cct cct cct tat ggt tct cca gag cct atg ggg ata aat acc agc tac	541
Pro Pro Pro Tyr Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr	
145 150 155	
ctg cag tct gtg gtg agc ccc tgc ggc ctc ata acc tct gga ggg gca	589

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Leu Gln Ser Val Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala
 160 165 170
 gca gcc gcc atg tca agt cct cct caa tac tac acc atc tac cct caa 637
 Ala Ala Ala Met Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln
 175 180 185
 gat aac tct gca ttt gtg gtt gat gag ggc tgc ctt tct ttc acg gac 685
 Asp Asn Ser Ala Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp
 190 195 200
 ggt gga aat cac agg ccc aat cct gat gtt gac cag cta gaa gag aca 733
 Gly Gly Asn His Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr
 205 210 215 220
 cag ctg gaa gag gag gcc tgt gcc tgc ttc tct cct ccc cct tat gaa 781
 Gln Leu Glu Glu Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu
 225 230 235
 gaa ata tac tct ctc cct cgc tagaggct attctgatat aataacacaa 830
 Glu Ile Tyr Ser Leu Pro Arg
 240
 tgctcagctc agggagcaag tgttccgctc attgttacct gacaaccgtg gtgttctatg 890
 ttgtaacctt cagaagttac agcagcgccc aggcagcctg acagagatca ttcaaggggg 950
 gaaaggggaa gtgggaggtg caatttctca gatttgtaaa aattaggctg ggctggggaa 1010
 attctcctcc ggaacagttt caaatccct cgggtaagaa atctcctgta taaggttcag 1070
 gagcaggaat ttcaactttt catccaccac cctccccctt ctctgtagga aggcattggt 1130
 ggctcaattt taaccccagc agccaatgga aaaatcacga cttctgagac ttggggagtt 1190
 tccacagagg tgagagtcgg gtgggaagga agcaggaag agaaagcagg ccagctgga 1250
 gatttctggt tggctgtcct tggcccaaaa gcagactcac taatcccaaa caactcagct 1310

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gccatctggc ctctctgagg actctgggta ccttaaagac tataaaacaa aacaaaacaa 1370
 aaacatcaaa ccaatgaaat aaaataaatc atgtctcctg ctagaatagt attggatacc 1430
 tgactaaatt acacaaaata gaccataata ggatagcact gtgaatacat ctttcccgat 1490
 cactgagtca cagtgaccct tggctgctgc agttctcgtc tgcaagggtg aagcttgacg 1550
 tgtgatgaac atgggtgggc tcttggtcca cccaggtg gggcctgcgc caagcatgaa 1610
 ctagctggga ccagtggctg acagaacaca ggacttcct aagtaccgt aggtccgtgg 1670
 agcaagacag agcagagttg ccatgtcaac acatggggaa tgataigata gaaacaatct 1730
 ttatgactaa aagaaactca tcttcttcat taaaaaaact ttggtgtcct t 1781

<210> 60

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (87)... (899)

<400> 60

attgggcggc gtgatctcgc cgcggttccg cggccctgcc gccgccgccg ccagcagagc 60
 gcaccgggcc gatcgggcga gtggcc atg gcg ggc gcc gag gac tgg ccg ggc 113

Met Ala Gly Ala Glu Asp Trp Pro Gly

1

5

cag cag ctg gag ctg gac gag gac gag gcg tct tgt tgc cgc tgg ggc 161

Gln Gln Leu Glu Leu Asp Glu Asp Glu Ala Ser Cys Cys Arg Trp Gly

10

15

20

25

gcg cag cac gcc ggg gcc cgc gag ctg gct gcg ctc tac tcg cca ggc 209

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Ala Gln His Ala Gly Ala Arg Glu Leu Ala Ala Leu Tyr Ser Pro Gly
 30 35 40
 aag cgc ctc cag gag tgg tgc tct gtg atc ctg tgc ttc agc ctc atc 257
 Lys Arg Leu Gln Glu Trp Cys Ser Val Ile Leu Cys Phe Ser Leu Ile
 45 50 55
 gcc cac aac ctg gtc cat ctc ctg ctg ctg gcc cgc tgg gag gac aca 305
 Ala His Asn Leu Val His Leu Leu Leu Leu Ala Arg Trp Glu Asp Thr
 60 65 70
 ccc ctc gtc ata ctc ggt gtt gtt gca ggg gct ctc att gct gac ttc 353
 Pro Leu Val Ile Leu Gly Val Val Ala Gly Ala Leu Ile Ala Asp Phe
 75 80 85
 ttg tct ggc ctg gta cac tgg ggt gct gac aca tgg ggc tct gtg gag 401
 Leu Ser Gly Leu Val His Trp Gly Ala Asp Thr Trp Gly Ser Val Glu
 90 95 100 105
 ctg ccc att gtg ggg aag gct ttc atc cga ccc ttc cgg gag cac cac 449
 Leu Pro Ile Val Gly Lys Ala Phe Ile Arg Pro Phe Arg Glu His His
 110 115 120
 att gac cca aca gct atc aca cgg cac gac ttc atc gag acc aac ggg 497
 Ile Asp Pro Thr Ala Ile Thr Arg His Asp Phe Ile Glu Thr Asn Gly
 125 130 135
 gac aac tgc ctg gtg aca ctg ctg ccg ctg cta aac atg gcc tac aag 545
 Asp Asn Cys Leu Val Thr Leu Leu Pro Leu Leu Asn Met Ala Tyr Lys
 140 145 150
 ttc cgc acc cac agc cct gaa gcc ctg gag cag cta tac ccc tgg gag 593
 Phe Arg Thr His Ser Pro Glu Ala Leu Glu Gln Leu Tyr Pro Trp Glu

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155	160	165	
tgc ttc gtc ttc tgc ctg atc atc ttc ggc acc ttc acc aac cag atc			641
Cys Phe Val Phe Cys Leu Ile Ile Phe Gly Thr Phe Thr Asn Gln Ile			
170	175	180	185
cac aag tgg tgc cac acg tac ttt ggg ctg cca cgc tgg gtc acc ctc			689
His Lys Trp Ser His Thr Tyr Phe Gly Leu Pro Arg Trp Val Thr Leu			
	190	195	200
ctg cag gac tgg cat gtc atc ctg cca cgt aaa cac cat cgc atc cac			737
Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His His Arg Ile His			
	205	210	215
cac gtc tca ccc cac gag acc tac ttc tgc atc acc aca ggc tgg ctc			785
His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr Thr Gly Trp Leu			
	220	225	230
aac tac cct ctg gag aag ata ggc ttc tgg cga cgc ctg gag gac ctc			833
Asn Tyr Pro Leu Glu Lys Ile Gly Phe Trp Arg Arg Leu Glu Asp Leu			
	235	240	245
atc cag ggc ctg acg ggc gag aag cct cgg gca gat gac atg aaa tgg			881
Ile Gln Gly Leu Thr Gly Glu Lys Pro Arg Ala Asp Asp Met Lys Trp			
250	255	260	265
gcc cag aag atc aaa taac ttctcggagc ctgctacctg gttgccaacc			930
Ala Gln Lys Ile Lys			
	270		
ttccctagcc cccaaaccga agccatctgc caaattccag cctctttgag ctggcccctc			990
cagatggaga ggacatctcc tgggctgggc ccaggtaccc cagcccaccc ctcatgacac			1050
agaatacttg agccactgat ttttcatttc tttttttttt tttttcctcg gccctcctc			1110

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agccacctga gttgctctat ctgcaagcct gactctgcca gcctcccctg gtagagagga 1170
 ggtttaccca ctccctgcac gcctgccgtc cctgccccgc tgggcagccc ttcagtgtgg 1230
 ctggcggttg ggccagttag ttgcctcttt ccctccttgt ctggccccag tggctctgggg 1290
 agcccccagg cacacctaaag cgtcgtggag cattgttctg ccacagccct gcatactgac 1350
 cccgggaggc tgggcagggtg gacagcccca gccaccacct tcagcctagc ctgtcccca 1410
 aggatggtga agctcagcag gggctctgagg gtagccggcc agaagaggct ggaacctcct 1470
 gctcaagtct agacccttac ttctctgtg cccccacct gccagagctg atgtttccaa 1530
 taccaagatg tcttcacagg gcacagcccc tgcagagcat cttggtcatt tggaagagga 1590
 cacggtatcc cctctggcca gagtatgtca gagaaggaag agtagggctt tttgttttg 1650
 ttttttttta aagggtcttg cttgtttaat gtaaataata gaaagcctta atatcttttc 1710
 tgtaacacgg agtaatatat taatgtcatg ttttgatgt acataatata tttataacaa 1770
 agcagcaaga gtctactt 1788

<210> 61

<211> 389

<212> PRT

<213> Homo sapiens

<400> 61

Met Asp Arg Gly Glu Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp

1

5

10

15

Trp Gly Thr Ser Phe Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe

20

25

30

Val Ser Pro Lys Gly Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val

35

40

45

Ser Leu Cys Val Trp Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr

138/307

50	55	60	
Leu Cys Ser Ala Glu Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln			
65	70	75	80
Tyr Tyr Phe Leu Lys Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn			
	85	90	95
Leu Trp Thr Ser Leu Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala			
	100	105	110
Leu Leu Leu Ala Glu Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser			
	115	120	125
Val Pro Lys Leu Pro Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile			
	130	135	140
Val Gly Ile Leu Thr Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln			
145	150	155	160
Ile Ala Ser Ser Val Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu			
	165	170	175
Thr Gly Val Val Phe Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg			
	180	185	190
Phe Gln Asn Ala Phe Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile			
	195	200	205
Gln Ala Ile Phe Gln Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys			
	210	215	220
Pro Arg Thr Thr Ile Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val			
225	230	235	240
Thr Val Val Tyr Leu Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr			
	245	250	255

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Pro Arg Glu Ile Leu Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp

260 265 270

Arg Ala Phe Pro Ser Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr

275 280 285

Ser Leu Phe Ser Asn Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro

290 295 300

Ile Tyr Leu Ala Ser Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr

305 310 315 320

Leu Asn Ser His Ser Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr

325 330 335

Leu Gly Ser Leu Ala Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn

340 345 350

Tyr Ile Phe Phe Thr Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly

355 360 365

Ile Leu Arg Arg Arg Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys

370 375 380

Val Lys Leu Asp Phe

385

<210> 62

<211> 348

<212> PRT

<213> Homo sapiens

<400> 62

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg

140/307

1	5	10	15
Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu			
20	25	30	
Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly Gln Thr Phe			
35	40	45	
Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val			
50	55	60	
Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val			
65	70	75	80
Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly			
85	90	95	
Ala Leu Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln			
100	105	110	
Val His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp			
115	120	125	
Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg Met Gln Pro Gly Pro Val			
130	135	140	
Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe Val Asp Thr			
145	150	155	160
Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser			
165	170	175	
Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly			
180	185	190	
Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His			
195	200	205	

141/307

Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile

210

215

220

Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val

225

230

235

240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser Ile

245

250

255

Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys Leu Phe

260

265

270

Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu His Arg Asp

275

280

285

Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu Met Thr Ala

290

295

300

Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile Val Phe Phe

305

310

315

320

Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile Ile Leu Tyr

325

330

335

Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr

340

345

<210> 63

<211> 261

<212> PRT

<213> Homo sapiens

<400> 63

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys

142/307

1	5	10	15
Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val			
20	25	30	
Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu			
35	40	45	
Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr			
50	55	60	
Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe			
65	70	75	80
Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg			
85	90	95	
Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu			
100	105	110	
Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr			
115	120	125	
Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro			
130	135	140	
Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr			
145	150	155	160
Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly			
165	170	175	
Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile			
180	185	190	
Leu Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val			
195	200	205	

143/307

Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro

210

215

220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu

225

230

235

240

Leu Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln

245

250

255

Gly Lys Thr Lys Asn

260

<210> 64

<211> 222

<212> PRT

<213> Homo sapiens

<400> 64

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu

1

5

10

15

Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg

20

25

30

Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr

35

40

45

Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg

50

55

60

Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg

65

70

75

80

Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu

144/307

85	90	95	
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile			
100	105	110	
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile			
115	120	125	
Pro Ser Thr Leu Ala Pro Pro Met Asp Pro Ser Val Pro Ile Trp Ile			
130	135	140	
Ile Ile Phe Gly Val Ile Phe Cys Ile Ile Ile Val Ala Ile Ala Leu			
145	150	155	160
Leu Ile Leu Ser Gly Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro			
165	170	175	
Ser Glu Val Asp Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile			
180	185	190	
Glu Asn Gly Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly His Ile			
195	200	205	
Asn Asp Ala Phe Met Thr Glu Asp Glu Arg Leu Thr Pro Leu			
210	215	220	

<210> 65

<211> 183

<212> PRT

<213> Homo sapiens

<400> 65

Met Gly Val Arg Val His Val Val Ala Ala Ser Ala Leu Leu Tyr Phe
1 5 10 15

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Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys Gly Asn Pro Glu

20

25

30

His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr Ile Trp Leu Leu

35

40

45

Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu Thr Ser Leu Cys

50

55

60

Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly Glu Asp Gly Gly

65

70

75

80

Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp His Asp Ser Thr

85

90

95

Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe Gly Pro Ala Ala

100

105

110

Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser Leu Gly Gln Leu

115

120

125

Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu Ala Leu His Met

130

135

140

Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala Pro Asp Leu Pro

145

150

155

160

Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu Lys Glu Ser Thr

165

170

175

Arg Ile Val Asp Ser Trp Asn

180

<210> 66

<211> 262

146/307

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn

1 5 10 15

Lys Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn

20 25 30

Tyr Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys

35 40 45

Glu Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly

50 55 60

Ser Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile

65 70 75 80

Pro Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val

85 90 95

Phe Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe

100 105 110

Phe Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser

115 120 125

Ser Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn

130 135 140

Ile Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln

145 150 155 160

Leu Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser

165 170 175

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Asn Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe

180

185

190

Tyr Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys

195

200

205

Thr Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly

210

215

220

Thr Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln

225

230

235

240

Ser Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln

245

250

255

Leu Thr Pro His Pro Pro

260

<210> 67

<211> 168

<212> PRT

<213> Homo sapiens

<400> 67

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser

1

5

10

15

Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro

20

25

30

Ser Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile

35

40

45

Thr Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys

148/307

50 55 60
 Leu Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser
 65 70 75 80
 Asn Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly
 85 90 95
 Ile Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
 100 105 110
 Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro
 115 120 125
 Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser
 130 135 140
 Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro
 145 150 155 160
 Asp Ser Pro Asn Phe Glu Val Ile

165

<210> 68

<211> 243

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val

1 5 10 15

Leu Leu Gly Val Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly

20 25 30

149/307

Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp
35 40 45
Gln Gln Ser Phe Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala
50 55 60
Trp Pro Gly Pro Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu
65 70 75 80
Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln
85 90 95
Asn Phe Ser Lys Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp
100 105 110
Pro Ile Ala Met Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro
115 120 125
Glu Asp Asp Asp Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln
130 135 140
Lys Thr Thr Glu Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys
145 150 155 160
Arg Gly Asp Leu Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser
165 170 175
Gly Leu Cys Pro Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp
180 185 190
Tyr Gln Asn Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val
195 200 205
Met Gly Gln Leu Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro
210 215 220
Asp Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala

150/307

225 230 235 240

Thr Glu Ala

<210> 69

<211> 428

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Ser Leu Cys Pro Gly Ala Trp Leu Arg Lys Pro Tyr Tyr

1 5 10 15

Leu Gln Ala Arg Phe Ser Tyr Val Arg Met Lys Tyr Leu Phe Phe Ser

20 25 30

Trp Leu Val Val Phe Val Gly Ser Trp Ile Ile Tyr Val Gln Tyr Ser

35 40 45

Thr Tyr Thr Glu Leu Cys Arg Gly Lys Asp Cys Lys Lys Ile Ile Cys

50 55 60

Asp Lys Tyr Lys Thr Gly Val Ile Asp Gly Pro Ala Cys Asn Ser Leu

65 70 75 80

Cys Val Thr Glu Thr Leu Tyr Phe Gly Lys Cys Leu Ser Thr Lys Pro

85 90 95

Asn Asn Gln Met Tyr Leu Gly Ile Trp Asp Asn Leu Pro Gly Val Val

100 105 110

Lys Cys Gln Met Glu Gln Ala Leu His Leu Asp Phe Gly Thr Glu Leu

115 120 125

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Glu Pro Arg Lys Glu Ile Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
 130 135 140
 Thr Val Gln Lys Phe Lys Glu Met Val Tyr Ser Leu Phe Lys Ala Lys
 145 150 155 160
 Leu Gly Asp Gln Gly Asn Leu Ser Glu Leu Val Asn Leu Ile Leu Thr
 165 170 175
 Val Ala Asp Gly Asp Lys Asp Gly Gln Val Ser Leu Gly Glu Ala Lys
 180 185 190
 Ser Ala Trp Ala Leu Leu Gln Leu Asn Glu Phe Leu Leu Met Val Ile
 195 200 205
 Leu Gln Asp Lys Glu His Thr Pro Lys Leu Met Gly Phe Cys Gly Asp
 210 215 220
 Leu Tyr Val Met Glu Ser Val Glu Tyr Thr Ser Leu Tyr Gly Ile Ser
 225 230 235 240
 Leu Pro Trp Val Ile Glu Leu Phe Ile Pro Ser Gly Phe Arg Arg Ser
 245 250 255
 Met Asp Gln Leu Phe Thr Pro Ser Trp Pro Arg Lys Ala Lys Ile Ala
 260 265 270
 Ile Gly Leu Leu Glu Phe Val Glu Asp Val Phe His Gly Pro Tyr Gly
 275 280 285
 Asn Phe Leu Met Cys Asp Thr Ser Ala Lys Asn Leu Gly Tyr Asn Asp
 290 295 300
 Lys Tyr Asp Leu Lys Met Val Asp Met Arg Lys Ile Val Pro Glu Thr
 305 310 315 320
 Asn Leu Lys Glu Leu Ile Lys Asp Arg His Cys Glu Ser Asp Leu Asp

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325	330	335	
Cys Val Tyr Gly Thr Asp Cys Arg Thr Ser Cys Asp Gln Ser Thr Met			
340	345	350	
Lys Cys Thr Ser Glu Val Ile Gln Pro Asn Leu Ala Lys Ala Cys Gln			
355	360	365	
Leu Leu Lys Asp Tyr Leu Leu Arg Gly Ala Pro Ser Glu Ile Arg Glu			
370	375	380	
Glu Leu Glu Lys Gln Leu Tyr Ser Cys Ile Ala Leu Lys Val Thr Ala			
385	390	395	400
Asn Gln Met Glu Met Glu His Ser Leu Ile Leu Asn Asn Leu Lys Thr			
405	410	415	
Leu Leu Trp Lys Lys Ile Ser Tyr Thr Asn Asp Ser			
420	425		

<210> 70

<211> 283

<212> PRT

<213> Homo sapiens

<400> 70

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

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Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys

50

55

60

Ser Leu Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser

65

70

75

80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly

85

90

95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

100

105

110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln

115

120

125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile

130

135

140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala

145

150

155

160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln

165

170

175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly

180

185

190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val

195

200

205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys

210

215

220

Leu Pro Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr

225

230

235

240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln

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	245		250		255										
Met	Thr	Ala	Ala	Ser	Arg	Cys	Pro	Arg	Arg	Phe	Ser	Gly	Thr	Cys	Gly
	260		265		270										
Arg	Arg	Lys	Arg	Lys	Arg	Leu	Leu	Trp	Ala	Ala					
	275		280												

<210> 71

<211> 1167

<212> DNA

<213> Homo sapiens

<400> 71

atggatagag gggagaaaat acagctcaag agagtgtttg gatattgggtg gggcacaagt	60
tttttgctta ttaatatcat tgggtgcagga atttttgtgt ccccaaagg tgtgttgga	120
tactcttgca tgaacgtggg agtctccctg tgcgtttggg ctggctgtgc catactggcc	180
atgacatcaa ctctttgctc tgcagagata agtataagct tccatgcag tggagctcaa	240
tactattttc tcaagagata ctttggtccc acggttgctt tttgaaatct ctggacatcc	300
ttgtttctgg ggtcaggggt agttgtggc caagctctgc tccttgctga gtacagcatc	360
cagccttttt tcccagctg ctctgtccca aagctgccta agaaatgtct ggcatggcc	420
atgttggtga ttgttagaat tctgacttct cgtgggtgtga aagaagtac ttggcttcag	480
atagctagct cagtgtgaa agtgtccata cttagcttca ttccctaac tggagtagtg	540
ttctgataa gagggaaaaa ggagaatgta gaacgatttc agaatgcttt tgatgtgaa	600
cttcagata tctctcacct tatacaagcc atctccaag gatattttgc atattcagg	660
gagctgaaga agcccagaac aacaattccc aatgcatat ttactgcgtt acctctggtg	720
actgtagttt atttactggt taacatttcc tatctgactg ttctgacacc cagggaatt	780
ctctcttcag atgctgtagc tatcacatgg gctgatcgag cttttccctc attagcatgg	840

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attatgcctt ttgctatttc tacctcatta tttagcaacc ttctgatttc tatatttaaa 900
 tcttcgagac caatatactt tgcaagccaa gagggccagc tgcctttgct atttaataca 960
 cttaatagtc actcttctcc atttacagct gtgctactac ttgtcacttt gggatccctt 1020
 gcaattatct taacaagtct aattgatttg ataaactata tttttttcac gggttcatta 1080
 tggctctatat tattaatgat aggaatacta aggcggagat accaggaacc caatctatct 1140
 ataccttata aggtaaaatt ggatttc 1167

<210> 72

<211> 1044

<212> DNA

<213> Homo sapiens

<400> 72

atggcggcga ctctgggacc ccttgggtcg tggcagcagt ggcggcgatg tttgtcggt 60
 cgggatgggt ccaggatgtt actccttctt cttttgttgg ggtctgggca ggggccacag 120
 caagtccggg cgggtcaaac gtctgagtac ttgaaacggg agcactcgct gtcgaagccc 180
 taccaggggtg tgggcacagg cagttcctca ctgtggaatc tgatgggcaa tgccatgggtg 240
 atgaccagct atatccgcct taccacagat atgcaaagta aacagggtgc cttgtggaac 300
 cgggtgccat gtttcctgag agactgggag ttgcaggtgc acttcaaat ccatggacaa 360
 ggaaagaaga atctgcatgg ggatggcttg gcaatctggt acacaaagga tcggatgcag 420
 ccagggcctg tgtttgaaa catggacaaa tttgtggggc tgggagtatt ttagacacc 480
 taccccaatg aggagaagca gcaagagcgg gtattccctt acatctcagc catggtgaac 540
 aacggctccc tcagctatga tcatgagcgg gatgggcggc ctacagagct gggaggctgc 600
 acagccattg tccgaatct tcattacgac accttcttgg tgattcgcta cgtcaagagg 660
 catttgacga taatgatgga tattgatggc aagcatgagt ggagggactg catigaagt 720
 cccggagtcc gcctgccccg cggtactac ttcggcacct cctccatcac tggggatctc 780

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tcagataatc atgatgtcat ttccttgaag ttgtttgaac tgacagtga gagaacccca	840
gaagaggaaa agctccatcg agatgtgttc ttgcctcag tggacaatat gaagctgcct	900
gagatgacag ctccactgcc gccctgagt ggcctggccc tcttcctcat cgtctttttc	960
tccctggtgt tttctgtatt tgccatagtc attggtatca tactctacaa caaatggcag	1020
gaacagagcc gaaagcgctt ctac	1044

<210> 73

<211> 783

<212> DNA

<213> Homo sapiens

<400> 73

atggaactgc ttcaagtgc cattcttttt cttctgccc gtatttgag cagtaacagc	60
acaggtgttt tagaggcagc taataattca cttgttgta ctacaacaaa accatctata	120
acaacaccaa acacagaatc attacagaaa aatgttgtca caccaacaac tggaacaact	180
cctaaaggaa caatcaccaa tgaattactt aaaatgtctc tgatgtcaac agctactttt	240
ttaacaagta aagatgaagg attgaaagcc acaaccactg atgtcaggaa gaatgactcc	300
atcatttcaa acgtaacagt aacaagtgtt acacttcaa atgctgtttc aacattacaa	360
agttccaaac ccaagactga aactcagagt tcaattaaaa caacagaaat accaggtagt	420
gttctacaac cagatgcac accttctaaa actggtacat taacctcaat accagttaca	480
attccagaaa acacctcaca gtctcaagta ataggcactg agggtgga aaatgcaagc	540
acttcagcaa ccagccggtc ttattccagt attattttgc cgggtggtat tgctttgatt	600
gtaataaacac tticagtatt tgttctggtg ggtttgtagc gaatgtgctg gaaggcagat	660
ccgggcacac cagaaaatgg aaatgatcaa cctcagtctg ataaagagag cgtgaagctt	720
cttaccgtta agacaatttc tcatgagtct ggtgagcact ctgcacaagg aaaaaccaag	780
aac	783

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<210> 74

<211> 666

<212> DNA

<213> Homo sapiens

<400> 74

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atgttgtggc tgctcttttt tctggtgact gccattcatg ctgaactctg tcaaccaggt      60
gcagaaaatg cttttaagt gagacttagt atcagaacag ctctgggaga taaagcatat      120
gcctgggata ccaatgaaga atacctcttc aaagcgatgg tagctttctc catgagaaaa      180
gttcccaaca gagaagcaac agaaatttcc catgtcctac tttgcaatgt aaccagagg      240
gtatcattct ggtttgtggt tacagaccct tcaaaaaatc acacccttcc tgctgttgag      300
gtgcaatcag ccataagaat gaacaagaac cggatcaaca atgccttctt tctaaatgac      360
caaactctgg aatttttaaa aatcccttcc acacttgac caccatgga cccatctgtg      420
cccatctgga ttattatatt tgggtgata ttttgcata tcatagttgc aattgcacta      480
ctgattttat cagggatctg gcaacgtaga agaaagaaca aagaaccatc tgaagtggat      540
gacgctgaag ataagtgtga aaacatgatc acaattgaaa atggcatccc ctctgatccc      600
ctggacatga agggagggca tattaatgat gccttcatga cagaggatga gaggtcacc      660
cctctc                                           666
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<210> 75

<211> 549

<212> DNA

<213> Homo sapiens

<400> 75

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atgggagtc gagttcatgt cgtggcggcc tcagccctgc tgtatttcat cctgctttct      60
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gggacgagat gtgaggaaaa ctgtggtaat cctgaacatt gcctgaccac agactgggta 120
catctctggt atatatgggt gctagtggta attggcgcgc tgcttctcct gtgtggcctg 180
acgtccctgt gcttccgctg ctgctgtctg agccgccagc aaaatgggga agatgggggc 240
ccaccaccct gtgaagtgac cgtcattgct ttcgatcacg acagcactct ccagagcact 300
atcacatctc tgcagtcggt gtttggccct gcagctcgga ggatcctggc tgtggctcac 360
tcccacagct ccttgggcca gctgcctcc tctttggaca cctcccagg gtatgaagaa 420
gctcttcaca tgagtcgctt cacagtagcc atgtgcgggc agaaagcacc tgatctaccc 480
ccagtacctg aagaaaagca gctgcctcca acagagaagg agtcgactcg aatagttgac 540
tcttggaac 549

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<210> 76

<211> 786

<212> DNA

<213> Homo sapiens

<400> 76

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atgggtaaga cgttttccca gctgggctct tggcgggagg atgagaacaa gtcaatcctg 60
tcctccaaac cagccattgg cagcaaggct gtcaactact ccagcaccgg tagcagcaag 120
tctttttgtt cctgtgtgcc ttgtgaagga actgctgatg ccagcttcgt gacttgtccc 180
acctgccagg gcagtggcaa gattccccaa gagctggaga agcagttggt ggctctcatt 240
ccctatgggg accagaggct gaagcccaag cacacgaagc tctttgtgtt cctggccgtg 300
ctcatctgcc tggtagacct ctccttcacg gtctttttcc tgtttcccg gtccgtcatt 360
gtgcagcctg caggcctcaa ctcctccaca gtggcctttg atgaggetga tatctacctc 420
aacataacga atatcttaaa catctccaat ggcaactact accccattat ggtgacacag 480
ctgaccctcg aggttctgca cctgtccctc gtgggtgggc aggtttccaa caaccttctc 540
ctacacattg gccctttggc cagtgaacag atgttttacg cagtagctac caagatacgg 600

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gatgaaaaca catacaaaat ctgtacctgg ctggaaatca aagtccacca tgtgcttttg 660
cacatccagg gcacctgac ctgttcatac ctgagccatt cagagcagct ggtctttcag 720
agctatgaat atgtggactg ccgaggaaac gcatctgtgc cccaccagct gacccctcac 780
ccacca 786

<210> 77

<211> 504

<212> DNA

<213> Homo sapiens

<400> 77

atgggcgtcc ccacggccct ggaggccggc agctggcgct ggggatccct gctcttcgct 60
ctcttcctgg ctgcgtccct aggcaaagat gcaccatcca actgtgtggt gtacccatcc 120
tcctcccagg agagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 180
ggaatcctct gcctccccct catcctgtct ctggtctaca agcaaaggca ggcagcctcc 240
aaccgccgtg cccaggagct ggtgcggatg gacagcaaca ttcaagggat tgaaaacccc 300
ggctttgaag cctcaccacc tgcccagggg atacccgagg ccaaagtcag gcacccctg 360
tcctatgtgg cccagcggca gccttctgag tctggcggc atctgcttcc ggagcccagc 420
acccccctgt ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 480
gactctcaa actttgaggt catc 504

<210> 78

<211> 729

<212> DNA

<213> Homo sapiens

<400> 78

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atgagctcgg ggactgaact gctgtggccc ggagcagcgc tgctggtgct gttgggggtg 60
 gcagccagtc tgtgtgtgcg ctgtcacgc ccagggtcaa agaggtcaga gaaaatctac 120
 cagcagagaa gtctgcgtga ggaccaacag agctttacgg ggtcccggac ctactccttg 180
 gtcgggcagg catggccagg acccctggcg gacatggcac ccacaaggaa ggacaagctg 240
 ttgcaattct accccagcct ggaggatcca gcactttcca ggtaccagaa cttcagcaaa 300
 ggaagcagac acgggtcgga ggaagcctac atagacccca ttgccatgga gtattacaac 360
 tggggggcgt tctcgaagcc cccagaagat gatgatgcca attcctacga gaatgtgctc 420
 atttgaagc agaaaaccac agagacaggt gccagcagg agggcatagg tggcctctgc 480
 agaggggacc tcagcctgtc actggccctg aagactggcc ccacttctgg tctctgtccc 540
 tctgcctccc cggaagaaga tgaggaatct gaggattatc agaactcagc atccatccat 600
 cagtggcgcg agtccaggaa ggtcatgggg caactccaga gagaagcatc ccctggcccg 660
 gtgggaagcc cagacgagga ggacggggaa ccggattacg tgaatgggga ggtggcagcc 720
 acagaagcc 729

<210> 79

<211> 1284

<212> DNA

<213> Homo sapiens

<400> 79

atggcgagga gtctctgtcc gggggcctgg ctaaggaaac cctattacct ccaggctcgc 60
 ttctcatatg tgcggatgaa atatcttttc ttttcttggt tagtggtttt tgttgaagc 120
 tggattatat atgtgcagta ttctacctat acagaattat gcagaggaaa ggactgtaag 180
 aaaataatat gtgacaagta caagactgga gttattgatg ggccctgcatg taacagcctt 240
 tgtgttacag aaactcttta ctttgaaaa tgtttatcca ccaagcccaa caatcagatg 300
 tatttaggga tttgggataa tctaccaggt gttgtgaaat gtcaaatgga acaagcgctt 360

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catcttgatt ttggaactga attggaacca agaaaagaaa tagtgctatt tgataagcca 420
actagaggaa ctactgtaca aaaattttaa gaaatggctct atagtctctt taaggcaaaa 480
ttgggtgacc aaggaaacct ctctgaactg gttaatctca tcttgacggt ggctgatgga 540
gacaaagatg gccaggttct cttgggagaa gcaaagtcgg catgggcact tcttcaactg 600
aatgaatttc ttctcatggt gatacttcaa gataaagaac ataccccaaa attaatggga 660
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ggatataatg ataagtatga ttgaaaatg gtggatatga gaaaaattgt gccagagaca 960
aacctgaaag aacttattaa ggatcgtcac tgtgagtctg atttggactg tgtctatggc 1020
acagattgta gaactagctg tgatcagagt acaatgaagt gtacttcaga agtgatacaa 1080
ccaaacttgg caaaagcttg tcagttactc aaagactacc tactgcgtgg tgctccaagt 1140
gaaattcgtg aagaattaga aaagcagctt tattcttgta ttgctctcaa agtcacagca 1200
aatcaaatgg aatggaaca ttctttgata ctaaataacc taaaaacatt attgtggaag 1260
aaaatttcct acactaatga ctct 1284

<210> 80

<211> 849

<212> DNA

<213> Homo sapiens

<400> 80

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gagcacactc tccggtacct ggtgctccac ctagcctccc tgcagctggg actgctgtta 180

162/307

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aacggggtct gcagcctggc tgaggagctg caccacatcc actccaggta ccggggcagc 240
tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg 300
ctgtccatct atttctacta ctecctccca aatgcggtcg gcccgccctt cacttgatg 360
cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc 420
ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggcca tgggctggca 480
tggtcatatt acatcgata tctgcggctg atcctgccag agctccaggc ccgattcga 540
acttacaatc agcattacaa caacctgcta cggggtgcag tgagccagcg gctgtatatt 600
ctctcccat tggactgtgg ggtgcctgat aacctgagta tggctgacc caacattcgc 660
ttcctggata aactgcccc gcagaccgct gaccgtgctg gcatcaagga tcgggtttac 720
agcaacagca tctatgagct tctggagaac gggcagcgga acctgcagat gacagcagct 780
tctcgtctc ccaggagggt ctccggcacc tgcggcagga ggaaaaggaa gaggttactg 840
tgggcagct 849

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<210> 81

<211> 1376

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (100)... (1269)

<400> 81

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attgtaattt atatagaatt ttaaaactct tcaattaca atg gat aga ggg gag 114

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Met Asp Arg Gly Glu

163/307

aaa ata cag ctc aag aga gtg ttt gga tat tgg tgg ggc aca agt ttt	162
Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp Trp Gly Thr Ser Phe	
10 15 20	
ttg ctt att aat atc att ggt gca gga att ttt gtg tcc ccc aaa ggt	210
Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe Val Ser Pro Lys Gly	
25 30 35	
gtg ttg gca tac tct tgc atg aac gtg gga gtc tcc ctg tgc gtt tgg	258
Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val Ser Leu Cys Val Trp	
40 45 50	
gct ggc tgt gcc ata ctg gcc atg aca tca act ctt tgc tct gca gag	306
Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr Leu Cys Ser Ala Glu	
55 60 65	
ata agt ata agc ttc cca tgc agt gga gct caa tac tat ttt ctc aag	354
Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln Tyr Tyr Phe Leu Lys	
70 75 80 85	
aga tac ttt ggc tcc acg gtt gct ttt ttg aat ctc tgg aca tcc ttg	402
Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn Leu Trp Thr Ser Leu	
90 95 100	
ttt ctg ggg tca ggg gta gtt gct ggc caa gct ctg ctc ctt gct gag	450
Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala Leu Leu Leu Ala Glu	
105 110 115	
tac agc atc cag cct ttt ttt ccc agc tgc tct gtc cca aag ctg cct	498
Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser Val Pro Lys Leu Pro	
120 125 130	
aag aaa tgt ctg gca ttg gcc atg ttg tgg att gta gga att ctg act	546

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Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile Val Gly Ile Leu Thr
 135 140 145
 tct cgt ggt gtg aaa gaa gtg act tgg ctt cag ata gct agc tca gtg 594
 Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln Ile Ala Ser Ser Val
 150 155 160 165
 ctg aaa gtg tcc ata ctt agc ttc att tcc cta act gga gta gtg ttc 642
 Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu Thr Gly Val Val Phe
 170 175 180
 ctg ata aga ggg aaa aag gag aat gta gaa cga ttt cag aat gct ttt 690
 Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg Phe Gln Asn Ala Phe
 185 190 195
 gat gct gaa ctt cca gat atc tct cac ctt ata caa gcc atc ttc caa 738
 Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile Gln Ala Ile Phe Gln
 200 205 210
 gga tat ttt gca tat tca ggg gag ctg aag aag ccc aga aca aca att 786
 Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys Pro Arg Thr Thr Ile
 215 220 225
 ccc aaa tgc ata ttt act gcg tta cct ctg gtg act gta gtt tat tta 834
 Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val Thr Val Val Tyr Leu
 230 235 240 245
 ctg gtt aac att tcc tat ctg act gtt ctg aca ccc agg gaa att ctc 882
 Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr Pro Arg Glu Ile Leu
 250 255 260
 tct tca gat gct gta gct atc aca tgg gct gat cga gct ttt ccc tca 930
 Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp Arg Ala Phe Pro Ser

165/307

265	270	275	
tta gca tgg att atg cct ttt gct att tct acc tca tta ttt agc aac			978
Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr Ser Leu Phe Ser Asn			
280	285	290	
ctt ctg att tct ata ttt aaa tct tcg aga cca ata tat ctt gca agc			1026
Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro Ile Tyr Leu Ala Ser			
295	300	305	
caa gag ggc cag ctg cct ttg cta ttt aat aca ctt aat agt cac tct			1074
Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr Leu Asn Ser His Ser			
310	315	320	325
tct cca ttt aca gct gtg cta cta ctt gtc act ttg gga tcc ctt gca			1122
Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr Leu Gly Ser Leu Ala			
330	335	340	
att atc tta aca agt cta att gat ttg ata aac tat att ttt ttc acg			1170
Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn Tyr Ile Phe Phe Thr			
345	350	355	
ggc tca tta tgg tct ata tta tta atg ata gga ata cta agg cgg aga			1218
Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly Ile Leu Arg Arg Arg			
360	365	370	
tac cag gaa ccc aat cta tct ata cct tat aag gta aaa ttg gat ttc			1266
Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys Val Lys Leu Asp Phe			
375	380	385	
taat tcttttctgt gtgaaataac agatattgag tataactgta tttaagatta			1320
taatcagagc atctataagt agatcttctg aatactcagt tactgtgaaa cacatg			1376

166/307

<210> 82

<211> 2392

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)... (1068)

<400> 82

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Met Ala Ala Thr Leu Gly Pro Leu Gly Ser

1

5

10

tgg cag cag tgg cgg cga tgt ttg tcg gct cgg gat ggg tcc agg atg 99

Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met

15

20

25

tta ctc ctt ctt ctt ttg ttg ggg tct ggg cag ggg cca cag caa gtc 147

Leu Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val

30

35

40

ggg gcg ggt caa acg ttc gag tac ttg aaa cgg gag cac tcg ctg tcg 195

Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser

45

50

55

aag ccc tac cag ggt gtg ggc aca ggc agt tcc tca ctg tgg aat ctg 243

Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu

60

65

70

atg ggc aat gcc atg gtg atg acc cag tat atc cgc ctt acc cca gat 291

Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp

167/307

75	80	85	90	
atg caa agt aaa cag ggt gcc ttg tgg aac cgg gtg cca tgt ttc ctg				339
Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe Leu				
	95	100	105	
aga gac tgg gag ttg cag gtg cac ttc aaa atc cat gga caa gga aag				387
Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly Lys				
	110	115	120	
aag aat ctg cat ggg gat ggc ttg gca atc tgg tac aca aag gat cgg				435
Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg				
	125	130	135	
atg cag cca ggg cct gtg ttt gga aac atg gac aaa ttt gtg ggg ctg				483
Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu				
	140	145	150	
gga gta ttt gta gac acc tac ccc aat gag gag aag cag caa gag cgg				531
Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg				
	155	160	165	170
gta ttc ccc tac atc tca gcc atg gtg aac aac ggc tcc ctc agc tat				579
Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr				
	175	180	185	
gat cat gag cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca gcc				627
Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala				
	190	195	200	
att gtc cgc aat ctt cat tac gac acc ttc ctg gtg att cgc tac gtc				675
Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val				
	205	210	215	

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aag agg cat ttg acg ata atg atg gat att gat ggc aag cat gag tgg	723
Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp	
220 225 230	
agg gac tgc att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac tac	771
Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Glu Tyr Tyr	
235 240 245 250	
ttc ggc acc tcc tcc atc act ggg gat ctc tca gat aat cat gat gtc	819
Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val	
255 260 265	
att tcc ttg aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa gag	867
Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu	
270 275 280	
gaa aag ctc cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag	915
Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys	
285 290 295	
ctg cct gag atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc ctc	963
Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu	
300 305 310	
ttc ctc atc gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata gtc	1011
Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val	
315 320 325 330	
att ggt atc ata ctc tac aac aaa tgg cag gaa cag agc cga aag cgc	1059
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg	
335 340 345	
ttc tac tgagc cctcctgctg ccaccacttt tgtgactgtc acctatgagg	1110

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Phe Tyr

tatggaagga gcaggcactg gcctgagcat gcagcctgga gagggttctt gtctctagca	1170
gctgggtggg gactatattc tgtcactgga gttttgaatg caggggacccc gcattcccat	1230
ggttgtgcat ggggacatct aactctggtc tgggaagcca cccaccccag ggcaatgctg	1290
ctgtgatgtg cttttccctg cagtccttcc atgtgggagc agagggtgtga agagaattta	1350
cgtgggtgtg atgccaaaat cacagaacag aatttcatag cccaggctgc cgtgttggtt	1410
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gggagatggc tttctgcttt ggatcactgt tccctagcat gggctcttggg tctattggca	1770
tgtccatggc cttcccaatc aagtctcttc aggccctcag tgaagtttgg ctaaaggttg	1830
gtgtaaaaat caagagaagc ctggaagaca tcatggatgc catggattag ctgtgcaact	1890
gaccagctcc aggtttgatc aaacaaaag caacatttgt catgttgtct gaccatgttg	1950
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170/307

<211> 1416

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55)... (840)

<400> 83

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Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser

5

10

15

agt aac agc aca ggt gtt tta gag gca gct aat aat tca ctt gtt gtt 153

Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val

20

25

30

act aca aca aaa cca tct ata aca aca cca aac aca gaa tca tta cag 201

Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln

35

40

45

aaa aat gtt gtc aca cca aca act gga aca act cct aaa gga aca atc 249

Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr Ile

50

55

60

65

acc aat gaa tta ctt aaa atg tct ctg atg tca aca gct act ttt tta 297

Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe Leu

70

75

80

171/307

aca agt aaa gat gaa gga ttg aaa gcc aca acc act gat gtc agg aag	345
Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg Lys	
85 90 95	
aat gac tcc atc att tca aac gta aca gta aca agt gtt aca ctt cca	393
Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu Pro	
100 105 110	
aat gct gtt tca aca tta caa agt tcc aaa ccc aag act gaa act cag	441
Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr Gln	
115 120 125	
agt tca att aaa aca aca gaa ata cca ggt agt gtt cta caa cca gat	489
Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro Asp	
130 135 140 145	
gca tca cct tct aaa act ggt aca tta acc tca ata cca gtt aca att	537
Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr Ile	
150 155 160	
cca gaa aac acc tca cag tct caa gta ata ggc act gag ggt gga aaa	585
Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly Lys	
165 170 175	
aat gca agc act tca gca acc agc cgg tct tat tcc agt att att ttg	633
Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile Leu	
180 185 190	
ccg gtg gtt att gct ttg att gta ata aca ctt tca gta ttt gtt ctg	681
Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val Leu	
195 200 205	
gtg ggt ttg tac cga atg tgc tgg aag gca gat ccg ggc aca cca gaa	729

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Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro Glu
 210 215 220 225
 aat gga aat gat caa cct cag tct gat aaa gag agc gtg aag ctt ctt 777
 Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu Leu
 230 235 240
 acc gtt aag aca att tct cat gag tct ggt gag cac tct gca caa gga 825
 Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln Gly
 245 250 255
 aaa acc aag aac tga cagcttgagg aattctctcc acacctaggc aataattacg 880
 Lys Thr Lys Asn
 260
 cttaatcttc agcttctatg caccaagcgt ggaaaaggag aaagtcctgc agaatcaatc 940
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<210> 84

<211> 1347

<212> DNA

<213> Homo sapiens

173/307

<220>

<221> CDS

<222> (26)... (694)

<400> 84

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Met Leu Trp Leu Leu Phe Phe Leu Val

1

5

act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat gct ttt 100

Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe

10

15

20

25

aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca tat gcc 148

Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala

30

35

40

tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct ttc tcc 196

Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser

45

50

55

atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat gtc cta 244

Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu

60

65

70

ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt aca gac 292

Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp

75

80

85

cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca gcc ata 340

Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile

90

95

100

105

174/307

aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat gac caa	388
Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp Gln	
110 115 120	
act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc atg gac	436
Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met Asp	
125 130 135	
cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt tgc atc	484
Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys Ile	
140 145 150	
atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg caa cgt	532
Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln Arg	
155 160 165	
aga aga aag aac aaa gaa cca tct gaa gtg gat gac gct gaa gat aag	580
Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Asp Lys	
170 175 180 185	
tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat ccc ctg	628
Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro Leu	
190 195 200	
gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag gat gag	676
Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp Glu	
205 210 215	
agg ctc acc cct ctc tgaagggt gttgttctgc ttctcaaga aattaaacat	730
Arg Leu Thr Pro Leu	
220	
ttgtttctgt gtgactgctg agcatcctga aataccaaga gcagatcata tattttgttt	790

175/307

caccattctt cttttgtaat aaattttgaa tgtgcttgaa agtgaaaagc aatcaattat 850
 acccaccaac accactgaaa tcataagcta ttcacgactc aaaatatctt aaaatatatt 910
 tctgacagta tagtgtataa atgtggatcat gtggtatttg tagttattga ttttaagcatt 970
 ttttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct aaggaaaaat 1030
 aaattttcca gtggagaata catataatat ggtgtagaaa tcattgaaaa tggatccttt 1090
 ttgacgatca cttatatcac tctgtatatg actaagtaaa caaaagtgag aagtaattat 1150
 tgtaaatgga tggataaaaa tggaattact catatacagg gtggaatttt atcctgttat 1210
 cacaccaaca gttgattata tattttctga atatcagccc ctaataggac aattctattt 1270
 gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa agtaataatc 1330
 atctcttttt gattgtg 1347

<210> 85

<211> 2284

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)... (626)

<400> 85

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 aggaattcag cccg atg gga gtc cga gtt cat gtc gtg gcg gcc tca gcc 110

Met Gly Val Arg Val His Val Val Ala Ala Ser Ala

1

5

10

ctg ctg tat ttc atc ctg ctt tct ggg acg aga tgt gag gaa aac tgt 158
 Leu Leu Tyr Phe Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys

176/307

15	20	25	
ggt aat cct gaa cat tgc ctg acc aca gac tgg gta cat ctc tgg tat			206
Gly Asn Pro Glu His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr			
30	35	40	
ata tgg ttg cta gtg gta att ggc gcg ctg ctt ctc ctg tgt ggc ctg			254
Ile Trp Leu Leu Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu			
45	50	55	60
acg tcc ctg tgc ttc cgc tgc tgc tgt ctg agc cgc cag caa aat ggg			302
Thr Ser Leu Cys Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly			
65	70	75	
gaa gat ggg ggc cca cca ccc tgt gaa gtg acc gtc att gct ttc gat			350
Glu Asp Gly Gly Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp			
80	85	90	
cac gac agc act ctc cag agc act atc aca tct ctg cag tcg gtg ttt			398
His Asp Ser Thr Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe			
95	100	105	
ggc cct gca gct cgg agg atc ctg gct gtg gct cac tcc cac agc tcc			446
Gly Pro Ala Ala Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser			
110	115	120	
ctg ggc cag ctg ccc tcc tct ttg gac acc ctc cca ggg tat gaa gaa			494
Leu Gly Gln Leu Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu			
125	130	135	140
gct ctt cac atg agt cgc ttc aca gta gcc atg tgc ggg cag aaa gca			542
Ala Leu His Met Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala			
145	150	155	

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cct gat cta ccc cca gta cct gaa gaa aag cag ctg cct cca aca gag	590
Pro Asp Leu Pro Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu	
160 165 170	
aag gag tcg act cga ata gtt gac tct tgg aac tgatgag agctgtcatt	640
Lys Glu Ser Thr Arg Ile Val Asp Ser Trp Asn	
175 180	
ttataaatag gagtggagtg atgtccagag tctgtgggaa aatggaacac atacttttct	700
aaccctcaga agttttaaga tggcatctaa caccatcatt ctatgggaaa gatggttctt	760
actcttcgtt cacaggcctt tatactctcc gatacagaat gctctaattg ggaactctaa	820
ttttgtatcc aatggccaaa atctgcaagt aatctctagc cacactgatt actactaaac	880
caggaaagca tcaaggtatc ttgaattcct ttaactattg agtgcataa gaattcctgt	940
accacatga tactgcaagt tgtgtctctc tctgtcagct aatccactgc ggttaactgg	1000
aaaagaaga caacagtgtc agcacagcca tcgacattaa tgcactgaat gcatgcatct	1060
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acataccac tcggatatct aaaagctagg gatggcattg ctgatatggg caaagagaac	1180
acagtatagt atttaagtgc caaatatcag tcttctttc tctctggtcc taccctcag	1240
cagtatgaaa aactccatac tgtgcagtca cagttggatt aattcttcag ttcctccgca	1300
ctgcaaacac atatatgtgc gcacatgat gtatactgc accctgtttt aactctaaag	1360
gaatagtgtt gctttacttc tttctgttt tgcctggacc acttaaagcc acaacacctc	1420
tatagtgaca cacgctagtc tctagtgggtg gccctcactg ccacctagag gagccatggt	1480
ggaaaacaca ctctctcctt tgagcctatc tgcacatctc tcgagttctt ggagcaaaaa	1540
ctaatgctg aactaagcct ggttgagatg cttcccatgg accatgccgc agcacagtgc	1600
taatctatcc acaaaacata ccacctcca aagtattatt attggaaaat cgaggaagtg	1660
acgcacattt agggaaaaac tactcacctt agaaaagtca ctgaaatcct tttttttttt	1720
tttgagatgg agttttgctc ttgtagccca ggctgggatg caatggcatg gtctcagctc	1780

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actgtaacct ccacctcccg gattcaagca attcttctgc ctcagcttcc cgactagctg 1840
 ggattacagc tgcctgccac cgtgcccagc taatttttgt attttttagtg gagagggggt 1900
 ttcacccatgt tggccagtct ggtctagaac tctgacgtc aggtgatccg cccaccttgg 1960
 cctcccaaag tgetggaatt agaggcctga cccctgctc ctggcctgaa atctttaaag 2020
 ccgttttttc cctaaaaaac gggaaataat aacacctcag aaggtttttg tgaagatcaa 2080
 agaagctaaa tatatgtggc atgatttgta aagtgttatg catatgtatg ttattcttcc 2140
 tactgtcttc taaccttccc ttgcctgcta tgacttatct gagagccatg ttcccattta 2200
 tctttttgcc aactatgtta ctgttgtcac acctgaaatg gctttgtttt tatcaataaa 2260
 tacttgttga ttgtggtaaa cagc 2284

<210> 86

<211> 1737

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (236)... (1024)

<400> 86

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 gccggcccca ggccgtgctt ctcccacca ccgccagct cagctcagcc cagcccagcc 120
 cactctgccc ttagaggccc ttctcccaa agacgcactc cagaagtctc gccctcgtgc 180
 ggctgaggag cctgggatcc cagacctgaa caagtgaac ccccgcccct gaaga atg 238

Met

1

ggt aag acg ttt tcc cag ctg ggc tct tgg cgg gag gat gag aac aag 286

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Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn Lys
 5 10 15
 tca atc ctg tcc tcc aaa cca gcc att ggc agc aag gct gtc aac tac 334
 Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn Tyr
 20 25 30
 tcc agc acc ggt agc agc aag tct ttt tgt tcc tgt gtg cct tgt gaa 382
 Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys Glu
 35 40 45
 gga act gct gat gcc agc ttc gtg act tgt ccc acc tgc cag ggc agt 430
 Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly Ser
 50 55 60 65
 ggc aag att ccc caa gag ctg gag aag cag ttg gtg gct ctc att ccc 478
 Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile Pro
 70 75 80
 tat ggg gac cag agg ctg aag ccc aag cac acg aag ctc ttt gtg ttc 526
 Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val Phe
 85 90 95
 ctg gcc gtg ctc atc tgc ctg gtg acc tcc tcc ttc atc gtc ttt ttc 574
 Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe Phe
 100 105 110
 ctg ttt ccc cgg tcc gtc att gtg cag cct gca ggc ctc aac tcc tcc 622
 Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser Ser
 115 120 125
 aca gtg gcc ttt gat gag gct gat atc tac ctc aac ata acg aat atc 670
 Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn Ile

180/307

130	135	140	145	
tta aac atc tcc aat ggc aac tac tac ccc att atg gtg aca cag ctg				718
Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln Leu				
	150	155	160	
acc ctc gag gtt ctg cac ctg tcc ctc gtg gtg ggg cag gtt tcc aac				766
Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser Asn				
	165	170	175	
aac ctt ctc cta cac att ggc cct ttg gcc agt gaa cag atg ttt tac				814
Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe Tyr				
	180	185	190	
gca gta gct acc aag ata cgg gat gaa aac aca tac aaa atc tgt acc				862
Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys Thr				
	195	200	205	
tgg ctg gaa atc aaa gtc cac cat gtg ctt ttg cac atc cag ggc acc				910
Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly Thr				
	210	215	220	225
ctg acc tgt tca tac ctg agc cat tca gag cag ctg gtc ttt cag agc				958
Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln Ser				
	230	235	240	
tat gaa tat gtg gac tgc cga gga aac gca tct gtg ccc cac cag ctg				1006
Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln Leu				
	245	250	255	
acc cct cac cca cca tgacctgtc tgetgtccct gtactccagg cacctgcaac				1060
Thr Pro His Pro Pro				

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cctggtctat atctcccaca actccctggt gactaaggaa ggactacaga ggctttgcca 1120
aaggagaagc cctgcctcat cacaccetta cctcccaccc cctcagcaca ggaagcttgc 1180
tttgaagtta acttcataca cacacactca tatcctccag ttccccccag attctttcag 1240
gggctgccat cagattctgc ccttggttag ttttttgttt ttttttttgg tagagacaga 1300
gtctcactgt tggtcagggt tggttttgaa ctctgggct caagcgatcc tcccttcttg 1360
gcctcccaaa gcacttgat tacagatgtg agcctgtgcc tggctggtct ttcttgagga 1420
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ctgtactgag cacctggtca gtctgaaggg ggcatctcac cccagctcca tcagggtg 1540
cagtccegtc tgaatgtgga gagagctgta gttttatctg gcttttaaaa catggacctg 1600
ccggctgggc gcagtggctt acacctgtaa tcccagtact ttgggaggcc gaagtgggtg 1660
gatcacttga gggcaggagt tcgtgaccag cctggtaaac atggtgaaac cttgtctcta 1720
ctaaaaatac aaaaatt 1737

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<210> 87

<211> 1556

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)... (609)

<400> 87

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gtccccggc accagaagtt cctctgcgcg tccgacggcg ac atg ggc gtc ccc 114

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Met Gly Val Pro

182/307

acg gcc ctg gag gcc ggc agc tgg cgc tgg gga tcc ctg ctc ttc gct	162
Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser Leu Leu Phe Ala	
5 10 15 20	
ctc ttc ctg gct gcg tcc cta ggc aaa gat gca cca tcc aac tgt gtg	210
Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro Ser Asn Cys Val	
25 30 35	
gtg tac cca tcc tcc tcc cag gag agt gaa aac atc acg gct gca gcc	258
Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr Ala Ala Ala	
40 45 50	
ctg gct acg ggt gcc tgc atc gta gga atc ctc tgc ctc ccc ctc atc	306
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu Ile	
55 60 65	
ctg ctc ctg gtc tac aag caa agg cag gca gcc tcc aac cgc cgt gcc	354
Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg Arg Ala	
70 75 80	
cag gag ctg gtg cgg atg gac agc aac att caa ggg att gaa aac ccc	402
Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile Glu Asn Pro	
85 90 95 100	
ggc ttt gaa gcc tca cca cct gcc cag ggg ata ccc gag gcc aaa gtc	450
Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val	
105 110 115	
agg cac ccc ctg tcc tat gtg gcc cag cgg cag cct tct gag tct ggg	498
Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser Glu Ser Gly	
120 125 130	
cgg cat ctg ctt tcg gag ccc agc acc ccc ctg tct cct cca ggc ccc	546

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Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro Pro Gly Pro

135

140

145

gga gac gtc ttc ttc cca tcc ctg gac cct gtc cct gac tct cca aac 594

Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp Ser Pro Asn

150

155

160

ttt gag gtc atc tagc ccagctgggg gacagtgggc tgttgtggct gggtctgggg 650

Phe Glu Val Ile

165

caggtgcatt tgagccaggg ctggctctgt gagtggcctc cttggcctcg gccctggttc 710

cctccctcct gctctgggct cagatactgt gacatcccag aagcccagcc cctcaacccc 770

tctggatgct acatggggat gctggacggc tcagcccctg ttccaaggat tttgggggtgc 830

tgagattctc ccctagagac ctgaaattca ccagctacag atgccaaatg acttacatct 890

taagaagtct cagaacgtcc agcccttcag cagctctcgt tctgagacat gagccttggg 950

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tgctcttctg tcagacttcc tctttgtacc acagtggctc tggggccagg cctgcctgcc 1130

cactggccat cgccaccttc ccagctgcc tctaccagc agtttctctg aagatctgtc 1190

aacaggttaa gtcaatctgg ggcttccact gcctgcattc cagtccccag agcttgggtg 1250

tcccgaacg ggaagtacat attggggcat ggtggcctcc gtgagcaa at ggtgtcttgg 1310

gcaatctgag gccaggacag atgttgcccc acccactgga gatggtgctg agggaggtgg 1370

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tactccact gctcagcgcg ggccattgca aggggtgccac acaatgtctt gtccaccctg 1490

ggacacttct gagtatgaag cgggatgcta ttaaaaacta catggggaaa caggtgcaaa 1550

ccctgg 1556

184/307

<210> 88

<211> 1855

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)... (953)

<400> 88

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ctccctgcct eggcctccca acgtgctggg attataggcg tgagccaccg ctccctggcca 120

gggtctgttc ctagttgcaa cagttcttgg aaaccactc gagagggcca cgcctccatt 180

caccaggcca cgcatacaca gaggcaacac caggagccaa c atg agc tcg ggg 233

Met Ser Ser Gly

1

act gaa ctg ctg tgg ccc gga gca gcg ctg ctg gtg ctg ttg ggg gtg 281

Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val Leu Leu Gly Val

5 10 15 20

gca gcc agt ctg tgt gtg cgc tgc tca cgc cca ggt gca aag agg tca 329

Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly Ala Lys Arg Ser

25 30 35

gag aaa atc tac cag cag aga agt ctg cgt gag gac caa cag agc ttt 377

Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp Gln Gln Ser Phe

40 45 50

acg ggg tcc cgg acc tac tcc ttg gtc ggg cag gca tgg cca gga ccc 425

Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala Trp Pro Gly Pro

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55	60	65	
ctg gcg gac atg gca ccc aca agg aag gac aag ctg ttg caa ttc tac			473
Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu Leu Gln Phe Tyr			
70	75	80	
ccc agc ctg gag gat cca gca tct tcc agg tac cag aac ttc agc aaa			521
Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln Asn Phe Ser Lys			
85	90	95	100
gga agc aga cac ggg tcg gag gaa gcc tac ata gac ccc att gcc atg			569
Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp Pro Ile Ala Met			
105	110	115	
gag tat tac aac tgg ggg cgg ttc tcg aag ccc cca gaa gat gat gat			617
Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro Glu Asp Asp Asp			
120	125	130	
gcc aat tcc tac gag aat gtg ctc att tgc aag cag aaa acc aca gag			665
Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln Lys Thr Thr Glu			
135	140	145	
aca ggt gcc cag cag gag ggc ata ggt ggc ctc tgc aga ggg gac ctc			713
Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys Arg Gly Asp Leu			
150	155	160	
agc ctg tca ctg gcc ctg aag act ggc ccc act tct ggt ctc tgt ccc			761
Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser Gly Leu Cys Pro			
165	170	175	180
tct gcc tcc ccg gaa gaa gat gag gaa tct gag gat tat cag aac tca			809
Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp Tyr Gln Asn Ser			
185	190	195	

186/307

gca tcc atc cat cag tgg cgc gag tcc agg aag gtc atg ggg caa ctc	857
Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val Met Gly Gln Leu	
200 205 210	
cag aga gaa gca tcc cct ggc ccg gtg gga agc cca gac gag gag gac	905
Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro Asp Glu Glu Asp	
215 220 225	
ggg gaa ccg gat tac gtg aat ggg gag gtg gca gcc aca gaa gcc	950
Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala Thr Glu Ala	
230 235 240	
tagggcagac caagaagaaa ggagccaagg caaagaggga ccactgtgct catggaccca	1010
tcgctgcctt ccaaggacca ttcccagag ctactcaact ttaagcccc tgccatgggt	1070
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gatttaggat aagctgtcac ccagtcccca taacaaaacc actgtccaac actggtatct	1310
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aatgattgat aagcttgtac agttaactta tagaggggga gccatattta acattctgga	1430
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ctgattaaac agtgttgtga ctgtctcatg ggaagagctg gggcccagag ggaccttgag	1790
tcagaaatgt tgccagaaaa agtatctcct ccaacaaaa catctcaata aaaccatttt	1850
agttg	1855

187/307

<210> 89

<211> 2530

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)... (1314)

<400> 89

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                                     1           5
gcc tgg cta agg aaa ccc tat tac ctc cag gct cgc ttc tca tat gtg      99
Ala Trp Leu Arg Lys Pro Tyr Tyr Leu Gln Ala Arg Phe Ser Tyr Val
      10           15           20
cgg atg aaa tat ctt ttc ttt tcc tgg tta gtg gtt ttt gtt gga agc      147
Arg Met Lys Tyr Leu Phe Phe Ser Trp Leu Val Val Phe Val Gly Ser
      25           30           35           40
tgg att ata tat gtg cag tat tct acc tat aca gaa tta tgc aga gga      195
Trp Ile Ile Tyr Val Gln Tyr Ser Thr Tyr Thr Glu Leu Cys Arg Gly
      45           50           55
aag gac tgt aag aaa ata ata tgt gac aag tac aag act gga gtt att      243
Lys Asp Cys Lys Lys Ile Ile Cys Asp Lys Tyr Lys Thr Gly Val Ile
      60           65           70
gat ggg cct gca tgt aac agc ctt tgt gtt aca gaa act ctt tac ttt      291

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188/307

Asp Gly Pro Ala Cys Asn Ser Leu Cys Val Thr Glu Thr Leu Tyr Phe
 75 80 85
 gga aaa tgt tta tcc acc aag ccc aac aat cag atg tat tta ggg att 339
 Gly Lys Cys Leu Ser Thr Lys Pro Asn Asn Gln Met Tyr Leu Gly Ile
 90 95 100
 tgg gat aat cta cca ggt gtt gtg aaa tgt caa atg gaa caa gcg ctt 387
 Trp Asp Asn Leu Pro Gly Val Val Lys Cys Gln Met Glu Gln Ala Leu
 105 110 115 120
 cat ctt gat ttt gga act gaa ttg gaa cca aga aaa gaa ata gtg cta 435
 His Leu Asp Phe Gly Thr Glu Leu Glu Pro Arg Lys Glu Ile Val Leu
 125 130 135
 ttt gat aag cca act aga gga act act gta caa aaa ttt aaa gaa atg 483
 Phe Asp Lys Pro Thr Arg Gly Thr Thr Val Gln Lys Phe Lys Glu Met
 140 145 150
 gtc tat agt ctc ttt aag gca aaa ttg ggt gac caa gga aac ctc tct 531
 Val Tyr Ser Leu Phe Lys Ala Lys Leu Gly Asp Gln Gly Asn Leu Ser
 155 160 165
 gaa ctg gtt aat ctc atc ttg acg gtg gct gat gga gac aaa gat ggc 579
 Glu Leu Val Asn Leu Ile Leu Thr Val Ala Asp Gly Asp Lys Asp Gly
 170 175 180
 cag gtt tcc ttg gga gaa gca aag tcg gca tgg gca ctt ctt caa ctg 627
 Gln Val Ser Leu Gly Glu Ala Lys Ser Ala Trp Ala Leu Leu Gln Leu
 185 190 195 200
 aat gaa ttt ctt ctc atg gtg ata ctt caa gat aaa gaa cat acc ccc 675
 Asn Glu Phe Leu Leu Met Val Ile Leu Gln Asp Lys Glu His Thr Pro

189/307

205	210	215	
aaa tta atg gga ttc tgt ggt gac ctc tat gtg atg gaa agt gtt gaa			723
Lys Leu Met Gly Phe Cys Gly Asp Leu Tyr Val Met Glu Ser Val Glu			
220	225	230	
tat acc tct ctt tat gga ata agc ctt cct tgg gtc att gaa ctt ttt			771
Tyr Thr Ser Leu Tyr Gly Ile Ser Leu Pro Trp Val Ile Glu Leu Phe			
235	240	245	
att cca tct ggg ttc aga aga agc atg gat cag ctg ttc aca cca tca			819
Ile Pro Ser Gly Phe Arg Arg Ser Met Asp Gln Leu Phe Thr Pro Ser			
250	255	260	
tgg cca aga aag gcc aaa ata gcc ata gga ctt cta gaa ttt gtg gaa			867
Trp Pro Arg Lys Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu			
265	270	275	280
gat gtt ttc cat ggc ccc tac gga aat ttc ctc atg tgc gat act agt			915
Asp Val Phe His Gly Pro Tyr Gly Asn Phe Leu Met Cys Asp Thr Ser			
285	290	295	
gcc aaa aac cta gga tat aat gat aag tat gat ttg aaa atg gtg gat			963
Ala Lys Asn Leu Gly Tyr Asn Asp Lys Tyr Asp Leu Lys Met Val Asp			
300	305	310	
atg aga aaa att gtg cca gag aca aac ctg aaa gaa ctt att aag gat			1011
Met Arg Lys Ile Val Pro Glu Thr Asn Leu Lys Glu Leu Ile Lys Asp			
315	320	325	
cgt cac tgt gag tct gat ttg gac tgt gtc tat ggc aca gat tgt aga			1059
Arg His Cys Glu Ser Asp Leu Asp Cys Val Tyr Gly Thr Asp Cys Arg			
330	335	340	

190/307

act agc tgt gat cag agt aca atg aag tgt act tca gaa gtg ata caa 1107
 Thr Ser Cys Asp Gln Ser Thr Met Lys Cys Thr Ser Glu Val Ile Gln
 345 350 355 360
 cca aac ttg gca aaa gct tgt cag tta ctc aaa gac tac cta ctg cgt 1155
 Pro Asn Leu Ala Lys Ala Cys Gln Leu Leu Lys Asp Tyr Leu Leu Arg
 365 370 375
 ggt gct cca agt gaa att cgt gaa gaa tta gaa aag cag ctt tat tct 1203
 Gly Ala Pro Ser Glu Ile Arg Glu Glu Leu Glu Lys Gln Leu Tyr Ser
 380 385 390
 tgt att gct ctc aaa gtc aca gca aat caa atg gaa atg gaa cat tct 1251
 Cys Ile Ala Leu Lys Val Thr Ala Asn Gln Met Glu Met Glu His Ser
 395 400 405
 ttg ata cta aat aac cta aaa aca tta ttg tgg aag aaa att tcc tac 1299
 Leu Ile Leu Asn Asn Leu Lys Thr Leu Leu Trp Lys Lys Ile Ser Tyr
 410 415 420
 act aat gac tct tagttcatt tggacataat taccatttta agaaacctgc 1350
 Thr Asn Asp Ser
 425
 cactttttaa gaacaatttt gagcattaaa aaaaaatggc ttcaaattcc tgccagttac 1410
 acaaaaactcc ttccccccag gcctgagaag ccatcagtat gtgattactg aagtaatggc 1470
 aggtgtagga tcaacaggtc cccaagatgt cattcctgcc cttttagaag ccctgttaca 1530
 tctccgaagt acattcattg tgtaactatt ttgactgact ttaaaaacca atgctgtgaa 1590
 aagcttcatt ccataaacat caacagtggag tgattttag atttaccta gccaaaatac 1650
 caatgctgga agcatttgtt ttgcattgaa gctgctgttc aacaagaaaa tttataaatt 1710
 tactaatgtc ttagcatggt aaagtttgca cattaacaga aattaagact gcaaagcagg 1770

191/307

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ttaaacttgc ttctttataa aacagatggt gggtaatat catggtttac tgtattaaag 1830
acttatacac ccatttttaa cctcattcag acatcaagtt atgtgtagct tcacaatggt 1890
tcaagtggct tacttcaaga aatcttatac ttgacagtac accaatttta ttgactaaaa 1950
atggatgaac tttcctaaag attcaaaggg cccatcttag tatcacgcag ctgactgagc 2010
cettcaaaac tgacatctta aggcccaatc aagatccaca taccctgatt ttgaactatg 2070
tgaaagtggg actgttaagt gcaagactaa aataaattat agcagacttt ttagtaataa 2130
ctttccattt tcaaacagta taccctgtgg gccaaagggc tatttcttaa agaggcatgt 2190
aaatgtatit atttatctaa tgtttttttc cccatgtaaa ctgatatac aaggtttagt 2250
atttgcctct ctttcatatt attttcacac gtatactcag atttggcatg tacctttcaa 2310
catctccata aaattaaaca ccttttgagg aaaagatcca ctattttctg ctcaaaggtt 2370
tcgcctacct aaagtgaac atgttaaaaa tctatgtgac catcactgga cagctttctc 2430
tcaaaacttt cttcaacgc catggattag caccagtttt gtttacttta aggtactttt 2490
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<210> 90

<211> 1911

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)... (1083)

<400> 90

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gtcctgtcga ggtgttaggt acagtgtgtt tgatcgtggt ggcttgaggg gaaccgctg 120
ttcagagctg tgactgcggc tgcaactcaga gaagctgccc ttggctgctc gtagcgccgg 180

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192/307

gccttctctc ctcgtcatca tccagagcag ccagtgtccg ggaggcagaa g atg ccc 237
Met Pro
1

cac tcc agc ctg cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc 285
His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala
5 10 15

cag aag gca gcc ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg 333
Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp
20 25 30

ggg cta gga gag cca cca gag cac act ctc cgg tac ctg gtg ctc cac 381
Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His
35 40 45 50

cta gcc tcc ctg cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg 429
Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu
55 60 65

gct gag gag ctg cac cac atc cac tcc agg tac cgg ggc agc tac tgg 477
Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp
70 75 80

agg act gtg cgg gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg 525
Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu
85 90 95

ttg ctg ctg tcc atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc 573
Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly
100 105 110

ccg ccc ttc act tgg atg ctt gcc ctc ctg ggc ctc tcg cag gca ctg 621

193/307

Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu
 115 120 125 130
 aac atc ctc ctg ggc ctc aag ggc ctg gcc cca gct gag atc tct gca 669
 Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala
 135 140 145
 gtg tgt gaa aaa ggg aat ttc aac gtg gcc cat ggg ctg gca tgg tca 717
 Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser
 150 155 160
 tat tac atc gga tat ctg cgg ctg atc ctg cca gag ctc cag gcc cgg 765
 Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg
 165 170 175
 att cga act tac aat cag cat tac aac aac ctg cta cgg ggt gca gtg 813
 Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val
 180 185 190
 agc cag cgg ctg tat att ctc ctc cca ttg gac tgt ggg gtg cct gat 861
 Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp
 195 200 205 210
 aac ctg agt atg gct gac ccc aac att cgc ttc ctg gat aaa ctg ccc 909
 Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro
 215 220 225
 cag cag acc gct gac cgt gct ggc atc aag gat cgg gtt tac agc aac 957
 Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn
 230 235 240
 agc atc tat gag ctt ctg gag aac ggg cag cgg aac ctg cag atg aca 1005
 Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln Met Thr

194/307

245	250	255	
gca gct tct cgc tgt ccc agg agg ttc tcc ggc acc tgc ggc agg agg			1053
Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly Arg Arg			
260	265	270	
aaa agg aag agg tta ctg tgg gca gct tgaagacctc agcgggtgccc			1100
Lys Arg Lys Arg Leu Leu Trp Ala Ala			
275	280		
agtacctcca cgatgtccca agagcctgag ctctcatca gtggaatgga aaagcccctc			1160
cctctccgca cggatttctc ttgagacca gggtcaccag gccagagcct ccagtgggtct			1220
ccaagcctct ggactggggg ctctcttcag tggctgaatg tccagcagag ctatttcctt			1280
ccacaggggg ccttgcaggg aagggtccag gacttgacat cttaatgatgc gtcttgtccc			1340
cttgggccag tcatttcccc tctctgagcc tcggtgtctt caacctgtga aatgggatca			1400
taatcactgc cttacctccc tcacggttgt tgtgaggact gagtgtgtgg aagtttttca			1460
taaactttgg atgctagtgt acttaggggg tgtgccaggt gtctttcatg gggccttcca			1520
gaccactcc ccaccttct ccccttcctt tgcccgggga cgcgaactc tctcaatggt			1580
atcaacaggc tccttcgccc tctggctcct ggtcatgttc cattattggg gagccccagc			1640
agaagaatgg agaggaggag gaggtgagt ttggggtatt gaatccccg gctccccccc			1700
tgcagcatca aggttgctat ggactctcct gccgggcaac tcttgcgtaa tcatgactat			1760
ctctaggatt ctggcaccac ttccttcctt ggccccttaa gcctagctgt gtatcggcac			1820
ccccaccca ctagagtact ccctctcact tgcgggttcc ttatactcca cccctttctc			1880
aacggctcctt ttttaaagca catctcagat t			1911

<210> 91

<211> 476

<212> PRT

195/307

<213> Homo sapiens

<400> 91

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met

1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser

20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr

35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly

50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65 70 75 80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln

85 90 95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro

100 105 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val

115 120 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr

130 135 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser

145 150 155 160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala

165 170 175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu

196/307

180	185	190	
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195	200	205	
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215	220	
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245	250	255	
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260	265	270	
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275	280	285	
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295	300	
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325	330	335	
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340	345	350	
Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys			
355	360	365	
Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn			
370	375	380	

197/307

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His Ser Leu

385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys

405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile

420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His

435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg

450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465 470 475

<210> 92

<211> 226

<212> PRT

<213> Homo sapiens

<400> 92

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val Gly Gly Phe

1 5 10 15

Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys Val Thr Thr

20 25 30

Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln Gly Leu Trp

35 40 45

Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys Arg Pro His

198/307

50	55	60	
Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys Arg Gly Leu			
65	70	75	80
Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile Phe Ala Leu			
	85	90	95
Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys Ala Lys Ala			
	100	105	110
Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser Gly Leu Cys			
	115	120	125
Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr Thr Glu Phe			
	130	135	140
Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly Ala Ala Leu			
145	150	155	160
Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly Gly Val Ile			
	165	170	175
Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg Tyr Thr Tyr			
	180	185	190
Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr His Gly Gly			
	195	200	205
Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp Lys Asn Ala			
	210	215	220
Tyr Val			
225			

<210> 93

199/307

<211> 305

<212> PRT

<213> Homo sapiens

<400> 93

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
1 5 10 15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
20 25 30
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
35 40 45
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
50 55 60
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
65 70 75 80
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
85 90 95
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
100 105 110
Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
115 120 125
Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
130 135 140
Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
145 150 155 160
Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala

200/307

	165	170	175
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu			
	180	185	190
Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys			
	195	200	205
Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu			
	210	215	220
Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp			
	225	230	235
Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe			
	245	250	255
Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp			
	260	265	270
Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys			
	275	280	285
His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr			
	290	295	300
Tyr			
305			

<210> 94

<211> 227

<212> PRT

<213> Homo sapiens

<400> 94

201/307

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
 1 5 10 15
 Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
 20 25 30
 Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
 35 40 45
 Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
 50 55 60
 Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
 65 70 75 80
 Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
 85 90 95
 Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
 100 105 110
 Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
 115 120 125
 Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
 130 135 140
 Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
 145 150 155 160
 Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
 165 170 175
 Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
 180 185 190
 Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala

202/307

195 200 205
 Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
 210 215 220
 Ala Ala Cys
 225

<210> 95

<211> 441

<212> PRT

<213> Homo sapiens

<400> 95

Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe
 1 5 10 15
 Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser
 20 25 30
 Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala
 35 40 45
 Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr
 50 55 60
 Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp
 65 70 75 80
 Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly
 85 90 95
 Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp
 100 105 110

203/307

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala
115 120 125
Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu
130 135 140
Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala
145 150 155 160
Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile
165 170 175
Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser
180 185 190
Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp
195 200 205
Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe
210 215 220
Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys
225 230 235 240
His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp
245 250 255
Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser
260 265 270
Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala
275 280 285
Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr
290 295 300
Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg

204/307

305 310 315 320
Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met
 325 330 335
Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys
 340 345 350
Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser
 355 360 365
Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu
 370 375 380
Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val
385 390 395 400
Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala
 405 410 415
Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln
 420 425 430
Val Phe Arg Asn Pro Tyr Val Trp Asp
 435 440

<210> 96

<211> 265

<212> PRT

<213> Homo sapiens

<400> 96

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys

1

5

10

15

205/307

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro

20

25

30

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val

35

40

45

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser

50

55

60

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser

65

70

75

80

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys

85

90

95

Ser Gly Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser

100

105

110

Gln Glu Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp

115

120

125

Leu Leu Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp

130

135

140

Asn Gly Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg

145

150

155

160

Asp Asp Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met

165

170

175

Glu Ile Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile

180

185

190

Glu Glu Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe

195

200

205

Cys Ile Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe

206/307

210	215	220	
Leu Leu Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr			
225	230	235	240
Val Glu Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser			
	245	250	255
Leu Lys Ile Thr Asn Asp Tyr Ile Phe			
	260	265	

<210> 97

<211> 208

<212> PRT

<213> Homo sapiens

<400> 97

Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala Val Phe			
1	5	10	15
Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala Val Leu			
	20	25	30
Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala Glu Gln			
	35	40	45
Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu Leu His			
	50	55	60
Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg Val Ala			
	65	70	75
His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu Arg Ala			
	85	90	95

207/307

His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser Leu Arg

100

105

110

Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp Asp Asp

115

120

125

Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp Gly Phe

130

135

140

Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr Ser Pro

145

150

155

160

Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro Pro Glu

165

170

175

Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala Ser Ser

180

185

190

Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys Asp Gln

195

200

205

<210> 98

<211> 400

<212> PRT

<213> Homo sapiens

<400> 98

Met Ala Trp Arg Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu

1

5

10

15

Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly

20

25

30

Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp

208/307

35	40	45	
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe			
50	55	60	
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro			
65	70	75	80
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe			
	85	90	95
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu			
100	105	110	
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala			
115	120	125	
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly			
130	135	140	
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val			
145	150	155	160
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln			
	165	170	175
Lys Gly Ile Pro Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val			
	180	185	190
Gln Glu Phe Ile Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe			
195	200	205	
Ile Thr Met Met Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile			
210	215	220	
Gln Arg Phe Leu Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg			
225	230	235	240

209/307

Lys Glu Thr Lys Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys
245 250 255
His Gly Glu Lys Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys
260 265 270
Ile Glu Asn Phe Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys
275 280 285
His Ile Phe His Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg
290 295 300
Thr Cys Pro Met Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp
305 310 315 320
Gly Glu Pro Gly Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro
325 330 335
Gly Arg Asp Pro Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp
340 345 350
Gly Ser Asp Glu Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu
355 360 365
Pro Gln Cys Asp Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala
370 375 380
Leu Leu Glu Ala Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser
385 390 395 400

<210> 99

<211> 192

<212> PRT

<213> Homo sapiens

210/307

<400> 99

Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp Tyr

1 5 10 15

Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr Val

20 25 30

His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr Glu

35 40 45

Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His

50 55 60

Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro

65 70 75 80

Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu Cys

85 90 95

Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln Gly

100 105 110

Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe Lys

115 120 125

Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu Met

130 135 140

Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser Thr

145 150 155 160

Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg

165 170 175

Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser Gly

180 185 190

211/307

<210> 100

<211> 260

<212> PRT

<213> Homo sapiens

<400> 100

Met Ala Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly

1 5 10 15

Leu Leu Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu

20 25 30

Cys Ala Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro

35 40 45

Pro Leu Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro

50 55 60

Arg Gly Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala

65 70 75 80

His Leu Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln

85 90 95

Glu Ala Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val

100 105 110

Trp Gly Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp

115 120 125

Pro Asp Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg

130 135 140

Leu Asp Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro

212/307

145 150 155 160
 Ala Ala Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala
 165 170 175
 Gly Pro Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro
 180 185 190
 Glu Leu Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp
 195 200 205
 Ser Glu Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His
 210 215 220
 Asp Val Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu
 225 230 235 240
 Arg Val Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg
 245 250 255
 Leu Leu Pro Pro
 260

<210> 101

<211> 1428

<212> DNA

<213> Homo sapiens

<400> 101

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 gatgggctgt ttgcgtccct atacagaagt gtttccatgc cacctaaggg agactcagga 120
 cagccattat ttctaccccc ttacattgaa gctgggaaga tccaaaaagg aagagaattg 180
 agtttggtcg gccctttccc aggactgaac atgaagagtt atgccggctt cctcaccgtg 240

213/307

aataagactt acaacagcaa cctcttcttc tggttcttcc cagctcagat acagccagaa 300
gatgccccag tagttctctg gctacagggt gggccgggag gttcatccat gtttggactc 360
tttgtggaac atgggcctta tgttgtcaca agtaacatga ccttgctga cagagacttc 420
ccctggacca caacgtctc catgctttac attgacaatc cagtgggcac aggcttcagt 480
tttactgatg ataccacagg atatgcagtc aatgaggacg atgtagcacg ggatttatac 540
agtgcactaa ttcagttttt ccagatatct cctgaatata aaaataatga cttttatgtc 600
actggggagt cttatgcagg gaaatatgtg ccagccattg cacacctcat ccattccctc 660
aaccctgtga gagaggtgaa gatcaacctg aacggaattg ctattggaga tggatattct 720
gatcccgaa caattatagg gggctatgca gaattcctgt accaaattgg cttgttgat 780
gagaagcaaa aaaagtactt ccagaagcag tgccatgaat gcatagaaca catcaggaag 840
cagaactgggt ttgaggcctt tgaaatactg gataaactac tagatggcga cttacaagt 900
gatccttctt acttccagaa tgttacagga ttagtaatt actataactt tttgcgggtc 960
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gaagatacag tacagtcagt taagccatgg ttaactgaaa tcatgaataa ttataaggtt 1140
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atgggcatgg actggaaagg atcccaggaa tacaagaagg cagaaaaaaa agtttgaag 1260
atctttaaat ctgacagtga agtggtggt tacatccggc aagcgggtga cttccatcag 1320
gtaattattc gaggtggagg acatatttta ccctatgacc agcctctgag agcttttgac 1380
atgattaatc gattcattta tggaaaagga tgggacctt atgttgga 1428

<210> 102

<211> 678

<212> DNA

<213> Homo sapiens

214/307

<400> 102

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gctgctacca cgtccaatga gtggaaagt accacgcgag cctcctcggg gataacagcc    120
acttgggttt accagggctt gtggatgaac tgcgcaggta acgcgttggg ttctttccat    180
tgccgaccgc attttactat ctcaaagta gcaggttata tacaggcatg tagaggactt    240
atgatcgtg ctgtcagcct gggcttcttt ggttccatat ttgcgctctt tggaatgaag    300
tgtaccaaag tcggaggctc cgataaagcc aaagctaaaa ttgcttgttt ggctgggatt    360
gtattcatat tgtcagggt gtgtcaatg actggatgtt ccctatatgc aaacaaaatc    420
acaacggaat tctttgatcc tctctttgtt gagcaaaagt atgaattagg agccgctctg    480
tttattggat gggcaggagc ctactgtgc ataattgggt gtgtcatatt ttgcttttca    540
atatctgaca acaacaaaac acccagatac acatacaacg gggccacatc tgtcatgtct    600
tctcggacaa agtatcatgg tggagaagat tttaaaacaa caaaccttc aaaacagttt    660
gataaaaatg cttatgtc                                     678

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<210> 103

<211> 915

<212> DNA

<213> Homo sapiens

<400> 103

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atggggatcc agacgagccc cgtcctgctg gcctccctgg ggggtggggt ggtcactctg    60
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ctggacccca atgaaaagta cctgctacga ctgctagaca agacgactgt gagccacaac    180
accaagaggt tccgctttgc cctgcccacc gccaccaca ctctggggct gcctgtgggc    240
aaacatatct acctctccac ccgaattgat ggcagcctgg tcacaggcc atacactcct    300
gtcaccagtg atgaggatca aggctatgtg gatcttgtca tcaaggtcta cctgaagggt    360

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215/307

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 ggggatgtgg tggagtttcg ggggccaagc gggttgctca cttacactgg aaaagggcatt 480
 tttaacattc agcccaacaa gaaatctcca ccagaacccc gagtggcgaa gaaactggga 540
 atgattgccg gcgggacagg aatcacccca atgctacagc tgatccgggc catcctgaaa 600
 gtccctgaag atccaaccca gtgctttctg ctttttgcca accagacaga aaaggatatc 660
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 ttcactctgg atcatcccc aaaagattgg gcctacagca agggctttgt gactgccgac 780
 atgatccggg aacacctgcc cgctccaggg gatgatgtgc tggtagtctt ttgtgggcca 840
 cccccaatgg tgcagctggc ctgccatccc aacttgga aactgggcta ctcacaaaag 900
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<210> 104

<211> 681

<212> DNA

<213> Homo sapiens

<400> 104

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 ctcttttgcc agggccttga agttttctac ccagagtgg ggaacattgg ctgcaaggtt 180
 gttctgatt gtaacaacta cagacagaag atcacctcct ggatggagcc gatagtcaag 240
 ttccggggg ccgtggacgg cgcaacctat atcctgttga tggtaggacc agatgccctt 300
 agcagagcag aaccagaca gagattctgg agacattggc tggtaacaga tatcaagggc 360
 gccgacctga agaaaggga gattcagggc caggagtat cagcctacca ggctccctcc 420
 ccaccggcac acagtggctt ccacgctac cagttcttgg tctatcttca ggaaggaaaa 480
 gtcattcttc tccttcccaa ggaaaacaaa actcgaggct cttggaaaaat ggacagattt 540

216/307

ctgaaccgtt tccacctggg cgaacctgaa gcaagcacc agtcatgac ccagaactac 600
caggactcac caacctcca ggctcccaga gaaagggcc ggcagccaa gcacaaaaac 660
caggcggaga tagctgcctg c 681

<210> 105

<211> 1323

<212> DNA

<213> Homo sapiens

<400> 105

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gcctggggccc agggccatgt cccaccggc tgcagccaag gcctcaacc cctgtactac 120
aacctgtgtg accgctctgg ggcgtggggc atcgctctgg aggccgtggc tggggcgggc 180
attgtcacca cgtttgtgct caccatcatc ctggtggcca gcctccctt tgtgcaggac 240
accaagaaac ggagcctgct ggggaccag gtattcttcc ttctggggac cctgggcctc 300
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ttctctttg gggttctgtt cgcatctgc ttctcttgtc tggcggctca cgtctttgcc 420
ctcaacttcc tggcccgaa gaaccacggg ccccggggct gggatgatt cactgtggct 480
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ccctgtgcca tcgccaacat ggactttgtc atggcactca tctacgtcat gctgctgctg 660
ctgggtgctt tctgggggc ctggccgcc ctgtgtggcc gctacaagcg ctggcgtaag 720
catgggtgtt ttgtgtcct caccacagcc acctccgtt ccatatgggt ggtgtggatc 780
gtcatgtata cttacggcaa caagcagcac aacagtccca cctgggatga cccacgctg 840
gccatgccc tcgcccga tgctgggcc ttctctctt tctacgtcat ccccgaggtc 900
tcccaggtga ccaagtccag cccagagcaa agctaccagg gggacatgta cccacccgg 960

217/307

ggcgtgggct atgagacat cctgaaagag cagaagggtc agagcatgtt cgtggagaac 1020
 aaggcctttt ccatggatga gccgggttga gctaagaggc cgggtgcacc atacagcggg 1080
 tacaatgggc agctgctgac cagtgtgtac cagcccactg agatggccct gatgcacaaa 1140
 gttccgtccg aaggagctta cgacatcatc ctcccacggg ccaccgcaa cagccaggtg 1200
 atgggcagtg ccaactcgac cctgcgggct gaagacatgt actcggcca gagccaccag 1260
 gcggccacac cgccgaaaga cggcaagaac tctcaggtct ttagaaacc ctacgtgtgg 1320
 gac 1323

<210> 106

<211> 795

<212> DNA

<213> Homo sapiens

<400> 106

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 tcggccatcc aagcccttgt ggggttggcg cggccgctgg tcttggcgt cctgcttgtg 120
 tccgccgctc tatccagtgt tgtatcacgg actgattcac cgagcccaac cgtactcaac 180
 tcacatattt ctaccccaaa tgtgaatgt ttaacacatg aaaaccaaac caaaccttct 240
 atttccaaa tcagcaccac cctccctccc acgacgagta ccaagaaaag tggaggagca 300
 tctgtggtec ctcatccctc gcctactcct ctgtctcaag aggaagctga taacaatgaa 360
 gatcctagta tagaggagga ggatcttctc atgctgaaca gttctccatc cacagccaaa 420
 gacactctag acaatggcga ttatggagaa ccagactatg actggaccac gggccccagg 480
 gacgacgacg agtctgatga caccttggaa gaaaacaggg gttacatgga aattgaacag 540
 tcagtgaat cttttaagat gccatcctca aatatagaag aggaagacag ccatttcttt 600
 tttcatctta ttattttgc tttttgcatt gctgttgttt acattacata tcacaacaaa 660
 aggaagattt ttcttctggt tcaaagcagg aaatggcgtg atggcctttg ttccaaaaca 720

218/307

gtggaatacc atcgccataga tcagaatgtt aatgaggcaa tgccttcttt gaagattacc 780
aatgattata ttttt 795

<210> 107

<211> 624

<212> DNA

<213> Homo sapiens

<400> 107

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gtccgtgacc tgcctagctga gcagcgcttc ccgggcccgcg tgcctgcctc ggacttggac 180
ctgctgttgc acatgaacaa cgcgcgtac ctgcgcgagg ccgactttgc gcgcgtcgcg 240
cacctgaccc gctgcggggg gctcggggcg ctgagggagt tgcggggcga cacggtgctg 300
gcggcctcgt gcgcgcgcca ccgccgctcg ctgcgcctgc tggagccctt cgaggtgcgc 360
accgcctgc tgggctggga cgaccgcgcg ttctacctgg aggcgcgctt tgctcagcctg 420
cgggacgggt tcgtgtgcgc gctgctgcgc ttccggcagc acctgctggg cacctcacc 480
gagcgcgtcg tgcagcacct gtgccagcgc aggggtggagc cccctgagct gcccgctgat 540
ctgcagcact ggatctccta caacgaggcc agcagccagc tgctccgcat ggagagtggg 600
ctcagtgatg tcaccaagga ccag 624

<210> 108

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 108

219/307

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ctcgccctgg ccctgtgcgt gcccggggcc cggggccggg ctctcgagtg gttctcggcc      120
gtggtaaaca tcgagtacgt ggacccgcag accaacctga cgggtgtggag cgtctcgag      180
agtggccgct tcggcgacag ctcgcccaag gagggcgcgc atggcctggt gggcgtcccg      240
tgggcgcccc gcggagacct cgagggtgc gcgccgaca cgcgttctt cgtgcccag      300
cccggcggcc gaggggcgc gccctgggtc gccctggttg ctctggtggg ctgcaccttc      360
aaggacaagg tgctgttggc ggcgcggagg aacgcctcgg ccgtcgtcct ctacaatgag      420
gagcgctacg ggaacatcac cttgcccattg tctcacgcgg gaacaggaaa tatagtggtc      480
attatgatta gctatccaaa aggaagagaa attttgagc tggtgcaaaa aggaattcca      540
gtaacgatga ccataggggt tggcaccgg catgtacagg agttcatcag cggtcagtct      600
gtggtgtttg tggccattgc ctcatcacc atgatgatta tctcgttagc ctggctaata      660
ttttactata tacagcgttt cctatatact ggctctcaga ttggaagtca gagccataga      720
aaagaaacta agaaagttat tggccagctt ctacttcata ctgtaaagca tggagaaaag      780
ggaattgatg ttgatgctga aaattgtgca gtgtgtattg aaaatttcaa agtaaaggat      840
attattagaa ttctgccatg caagcatatt ttcatagaa tatgcattga cccatggctt      900
ttggatcacc gaacatgtcc aatgtgtaaa cttgatgtca tcaaagccct aggatattgg      960
ggagagcctg gggatgtaca ggagatgcct gtcacagaat ctctccttg aagggatcca     1020
gctgcaaatt tgagtctagc ttaccagat gatgacggaa gtgatgagag cagtccacca     1080
tcagcctccc ctgctgaatc tgagccacag tgtgatccca gctttaaagg agatgcagga     1140
gaaaatacgg cattgctaga agccggcagg agtgactctc ggcatggagg acctatctcc     1200

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<210> 109

<211> 576

<212> DNA

<213> Homo sapiens

220/307

<400> 109

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ggatgtgttt tccagagcac agaagacaaa tgtatattca agatagactg gactctgtca	180
ccaggagagc acgccaagga cgaatatgtg ctatactatt actccaatct cagtgtgcct	240
attgggcgct tccagaaccg cgtacacttg atgggggaca acttatgcaa tgatggctct	300
ctcctgtctc aagatgtgca agaggctgac cagggaacct atatctgtga aatccgcctc	360
aaaggggaga gccaggtgtt caagaaggcg gtggtactgc atgtgcttcc agaggagccc	420
aaagagctca tgggtccatgt ggggtggattg attcagatgg gatgtgtttt ccagagcaca	480
gaagtgaac acgtgaccaa ggtagaatgg atattttcag gacggcgcgc aaaggttaaca	540
aggaggaaac atcactgtgt tagagaaggc tctggc	576

<210> 110

<211> 780

<212> DNA

<213> Homo sapiens

<400> 110

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ctgtgctcgc gcctgtttcg gccgcccccc gcgctctgcg cgcggccggt aaaggagccc	120
cgcggcctaa gcgcagcgtc tccgcccttg gctgagactg gcgctcctcg ccgcttccgg	180
cggtcagtgc cccgaggtga ggccggcgggg gcggtgcagg agctggcgcg ggcgctggcg	240
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cagcaggcgc gcgtcctggc gcagctgctg cgcgtctggg gcgcccccg caactctgat	360
ccggctctgg gcctggacga cgaccccgac gcgcctgcag cgcagctcgc tcgcgtctg	420
ctccgcgcc gccttgacc tgccgccctc gcagcccage ttgtccccgc gcccgcccc	480

221/307

gcccgcggcgc tccgaccccg gcccccggtc tacgacgacg gccccgcggg cccggatgct 540
gaggaggcag gcgacgagac acccgacgtg gaccccgagc tggtgaggta cttgctggga 600
cggattcttg cgggaagcgc ggactccgag ggggtggcag ccccgcgccg cctccgccgt 660
gccgccgacc acgatgtggg ctctgagctg ccccctgagg gcgtgctggg ggcgctgctg 720
cgtgtgaaac gcctagagac cccggcgccc caggtgcctg cacgccgct cttgccaccc 780

<210> 111

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (68)... (1498)

<400> 111

acaaccggct ggggtccttg cgcgccgcgg ctcaggagg agcaccgact gcgccgcacc 60
ctgagag atg gtt ggt gcc atg tgg aag gtg att gtt tcg ctg gtc ctg 109
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu
1 5 10
ttg atg cct ggc ccc tgt gat ggg ctg ttt cgc tcc cta tac aga agt 157
Leu Met Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser
15 20 25 30
gtt tcc atg cca cct aag gga gac tca gga cag cca tta ttt ctc acc 205
Val Ser Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr
35 40 45
cct tac att gaa gct ggg aag atc caa aaa gga aga gaa ttg agt ttg 253

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Pro Tyr Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu
 50 55 60
 gtc ggc cct ttc cca gga ctg aac atg aag agt tat gcc ggc ttc ctc 301
 Val Gly Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu
 65 70 75
 acc gtg aat aag act tac aac agc aac ctc ttc ttc tgg ttc ttc cca 349
 Thr Val Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro
 80 85 90
 gct cag ata cag cca gaa gat gcc cca gta gtt ctc tgg cta cag ggt 397
 Ala Gln Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly
 95 100 105 110
 ggg ccg gga ggt tca tcc atg ttt gga ctc ttt gtg gaa cat ggg cct 445
 Gly Pro Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro
 115 120 125
 tat gtt gtc aca agt aac atg acc ttg cgt gac aga gac ttc ccc tgg 493
 Tyr Val Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp
 130 135 140
 acc aca acg ctc tcc atg ctt tac att gac aat cca gtg ggc aca ggc 541
 Thr Thr Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly
 145 150 155
 ttc agt ttt act gat gat acc cac gga tat gca gtc aat gag gac gat 589
 Phe Ser Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp
 160 165 170
 gta gca cgg gat tta tac agt gca cta att cag ttt ttc cag ata ttt 637
 Val Ala Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe

223/307

175	180	185	190	
cct gaa tat aaa aat aat gac ttt tat gtc act ggg gag tct tat gca				685
Pro Glu Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala				
	195	200	205	
ggg aaa tat gtg cca gcc att gca cac ctc atc cat tcc ctc aac cct				733
Gly Lys Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro				
	210	215	220	
gtg aga gag gtg aag atc aac ctg aac gga att gct att gga gat gga				781
Val Arg Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly				
	225	230	235	
tat tct gat ccc gaa tca att ata ggg ggc tat gca gaa ttc ctg tac				829
Tyr Ser Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr				
	240	245	250	
caa att ggc ttg ttg gat gag aag caa aaa aag tac ttc cag aag cag				877
Gln Ile Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln				
	255	260	265	270
tgc cat gaa tgc ata gaa cac atc agg aag cag aac tgg ttt gag gcc				925
Cys His Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala				
	275	280	285	
ttt gaa ata ctg gat aaa cta cta gat ggc gac tta aca agt gat cct				973
Phe Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro				
	290	295	300	
tct tac ttc cag aat gtt aca gga tgt agt aat tac tat aac ttt ttg				1021
Ser Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu				
	305	310	315	

224/307

cgg tgc acg gaa cct gag gat cag ctt tac tat gtg aaa ttt ttg tca	1069
Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser	
320 325 330	
ctc cca gag gtg aga caa gcc atc cac gtg ggg aat cag act ttt aat	1117
Leu Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn	
335 340 345 350	
gat gga act ata gtt gaa aag tac ttg cga gaa gat aca gta cag tca	1165
Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser	
355 360 365	
gtt aag cca tgg tta act gaa atc atg aat aat tat aag gtt ctg atc	1213
Val Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile	
370 375 380	
tac aat ggc caa ctg gac atc atc gtg gca gct gcc ctg aca gag cac	1261
Tyr Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His	
385 390 395	
tcc ttg atg ggc atg gac tgg aaa gga tcc cag gaa tac aag aag gca	1309
Ser Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala	
400 405 410	
gaa aaa aaa gtt tgg aag atc ttt aaa tct gac agt gaa gtg gct ggt	1357
Glu Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly	
415 420 425 430	
tac atc cgg caa gcg ggt gac ttc cat cag gta att att cga ggt gga	1405
Tyr Ile Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly	
435 440 445	
gga cat att tta ccc tat gac cag cct ctg aga gct ttt gac atg att	1453

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Gly His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile

450

455

460

aat cga ttc att tat gga aaa gga tgg gat cct tat gtt gga taaac 1500

Asn Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465

470

475

taccttccca aaagagaaca tcagaggttt tcattgctga aaagaaaatc gtaaaaacag 1560

aaaatgtcat aggaataaaa aaattatctt ttcatatctg caagattttt ttcataata 1620

aaaattatcc ttg 1633

<210> 112

<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)... (872)

<400> 112

ctttaaaatg tcattggtaa accatacttg atcctaaatt cctgtacttc ctcaggccat 60

ccgagcatga aacgctgtca cctaccacaca tccgctggct gtgacgcttg tcaaagtgtt 120

ctctatcggc tgcattgccta gaccacaaaa gcgttctgac cggacagtgt cactggagaa 180

ggcggcgaga c atg tcc agg gcg cag atc tgg gct ctg gtg tct ggt gtc 230

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val

1

5

10

gga ggg ttt gga gct ctc gtt gct gct acc acg tcc aat gag tgg aaa 278

Gly Gly Phe Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys

226/307

15	20	25	
gtg acc acg cga gcc tcc tcg gtg ata aca gcc act tgg gtt tac cag			326
Val Thr Thr Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln			
30	35	40	45
ggg ctg tgg atg aac tgc gca ggt aac gcg ttg ggt tct ttc cat tgc			374
Gly Leu Trp Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys			
50	55	60	
cga ccg cat ttt act atc ttc aaa gta gca ggt tat ata cag gca tgt			422
Arg Pro His Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys			
65	70	75	
aga gga ctt atg atc gct gct gtc agc ctg ggc ttc ttt ggt tcc ata			470
Arg Gly Leu Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile			
80	85	90	
ttt gcg ctc ttt gga atg aag tgt acc aaa gtc gga ggc tcc gat aaa			518
Phe Ala Leu Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys			
95	100	105	
gcc aaa gct aaa att gct tgt ttg gct ggg att gta ttc ata ctg tca			566
Ala Lys Ala Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser			
110	115	120	125
ggg ctg tgc tca atg act gga tgt tcc cta tat gca aac aaa atc aca			614
Gly Leu Cys Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr			
130	135	140	
acg gaa ttc ttt gat cct ctc ttt gtt gag caa aag tat gaa tta gga			662
Thr Glu Phe Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly			
145	150	155	

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gcc gct ctg ttt att gga tgg gca gga gcc tca ctg tgc ata att ggt 710
 Ala Ala Leu Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly
 160 165 170
 ggt gtc ata ttt tgc ttt tca ata tct gac aac aac aaa aca ccc aga 758
 Gly Val Ile Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg
 175 180 185
 tac aca tac aac ggg gcc aca tct gtc atg tct tct cgg aca aag tat 806
 Tyr Thr Tyr Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr
 190 195 200 205
 cat ggt gga gaa gat ttt aaa aca aca aac cct tca aaa cag ttt gat 854
 His Gly Gly Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp
 210 215 220
 aaa aat gct tat gtc t aaaagagctc gcgggcaagc tgctcttga 900
 Lys Asn Ala Tyr Val
 225
 gtttggtata aaagcgaact gttcacaaaa tgatcccatc aaggccctcc cataattaac 960
 actcaaaact atttttaaaa tatgcatttg aagcatctgt tgattgtatg gatgtaagtg 1020
 ttcttacata gttagttata tactaatcat tttctgttgt ggctttctat aaaaaataaa 1080
 cagtttatatt acagg 1095

<210> 113

<211> 1602

<212> DNA

<213> Homo sapiens

<220>

228/307

<221> CDS

<222> (34)... (951)

<400> 113

ttgtcaggt ggtggaggaa aaggcgtcc gtc atg ggg atc cag acg agc ccc	54
Met Gly Ile Gln Thr Ser Pro	
1 5	
gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg	102
Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu	
10 15 20	
gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act	150
Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr	
25 30 35	
ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg cta gac aag acg	198
Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr	
40 45 50 55	
act gtg agc cac aac acc aag agg ttc cgc ttt gcc ctg ccc acc gcc	246
Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala	
60 65 70	
cac cac act ctg ggg ctg cct gtg ggc aaa cat atc tac ctc tcc acc	294
His His Thr Leu Gly Leu Pro Val Gly Lys His Ile Tyr Leu Ser Thr	
75 80 85	
cga att gat ggc agc ctg gtc atc agg cca tac act cct gtc acc agt	342
Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr Pro Val Thr Ser	
90 95 100	
gat gag gat caa ggc tat gtg gat ctt gtc atc aag gtc tac ctg aag	390

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Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Ile Lys Val Tyr Leu Lys
 105 110 115
 ggt gtg cac ccc aaa ttt cct gag gga ggg aag atg tct cag tac ctg 438
 Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met Ser Gln Tyr Leu
 120 125 130 135
 gat agc ctg aag gtt ggg gat gtg gtg gag ttt cgg ggg cca agc ggg 486
 Asp Ser Leu Lys Val Gly Asp Val Val Glu Phe Arg Gly Pro Ser Gly
 140 145 150
 ttg ctc act tac act gga aaa ggg cat ttt aac att cag ccc aac aag 534
 Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile Gln Pro Asn Lys
 155 160 165
 aaa tct cca cca gaa ccc cga gtg gcg aag aaa ctg gga atg att gcc 582
 Lys Ser Pro Pro Glu Pro Arg Val Ala Lys Lys Leu Gly Met Ile Ala
 170 175 180
 ggc ggg aca gga atc acc cca atg cta cag ctg atc cgg gcc atc ctg 630
 Gly Gly Thr Gly Ile Thr Pro Met Leu Gln Leu Ile Arg Ala Ile Leu
 185 190 195
 aaa gtc cct gaa gat cca acc cag tgc ttt ctg ctt ttt gcc aac cag 678
 Lys Val Pro Glu Asp Pro Thr Gln Cys Phe Leu Leu Phe Ala Asn Gln
 200 205 210 215
 aca gaa aag gat atc atc ttg cgg gag gac tta gag gaa ctg cag gcc 726
 Thr Glu Lys Asp Ile Ile Leu Arg Glu Asp Leu Glu Glu Leu Gln Ala
 220 225 230
 cgc tat ccc aat cgc ttt aag ctc tgg ttc act ctg gat cat ccc cca 774
 Arg Tyr Pro Asn Arg Phe Lys Leu Trp Phe Thr Leu Asp His Pro Pro

230/307

235	240	245	
aaa gat tgg gcc tac agc aag ggc ttt gtg act gcc gac atg atc cgg			822
Lys Asp Trp Ala Tyr Ser Lys Gly Phe Val Thr Ala Asp Met Ile Arg			
250	255	260	
gaa cac ctg ccc gct cca ggg gat gat gtg ctg gta ctg ctt tgt ggg			870
Glu His Leu Pro Ala Pro Gly Asp Asp Val Leu Val Leu Leu Cys Gly			
265	270	275	
cca ccc cca atg gtg cag ctg gcc tgc cat ccc aac ttg gac aaa ctg			918
Pro Pro Pro Met Val Gln Leu Ala Cys His Pro Asn Leu Asp Lys Leu			
280	285	290	295
ggc tac tca caa aag atg cga ttc acc tac tg agcatcctcc agcttcctg			970
Gly Tyr Ser Gln Lys Met Arg Phe Thr Tyr			
300	305		
gtgctgttcg ctgcagttgt tccccatcag tactcaagca ctataagcct tagattcctt			1030
tcctcagagt ttcaggtttt ttcagttaca tctagagctg aaatctggat agtacctgca			1090
ggaacaatat tcctgtagcc atggaagagg gccaaaggctc agtcactcct tggatggcct			1150
cctaaatctc cccgtggcaa caggctccagg agaggcccat ggagcagtct cttccatgga			1210
gtaagaagga agggagcatg tacgcttggt ccaagattgg ctagttcctt gatagcatct			1270
tactctcacc ttctttgtgt ctgtgatgaa aggaacagtc tgtgcaatgg gttttactta			1330
aacttcactg ttcaacctat gagcaaactct gtatgtgtga gtataagttg agcatagcat			1390
acttcagag gtggtcttat ggagatggca agaaaggagg aaatgatttc ttcagatctc			1450
aaaggagtct gaaatatcat atttctgtgt gtgtctctct cagcccctgc ccaggctaga			1510
gggaaacagc tactgataat cgaaaactgc tgtttgtggc aggaaccctt ggctgtgcaa			1570
ataaatgggg ctgaggcccc tgttgtatat tg			1602

231/307

<210> 114

<211> 897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99)... (782)

<400> 114

agtcctccca aagtacttgt gtccgggtgg tggactggat tcgctgcgga gccctggaag 60

ctgcctttcc ttctccctgt gcttaaccag aggtgccc atg ggt tgg aca atg 113

Met Gly Trp Thr Met

1

5

agg ctg gtc aca gca gca ctg tta ctg ggt ctc atg atg gtg gtc act 161

Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu Met Met Val Val Thr

10

15

20

gga gac gag gat gag aac agc ccg tgt gcc cat gag gcc ctc ttg gac 209

Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His Glu Ala Leu Leu Asp

25

30

35

gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac cca gag ttg 257

Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro Glu Leu

40

45

50

ggg aac att ggc tgc aag gtt gtt cct gat tgt aac aac tac aga cag 305

Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys Asn Asn Tyr Arg Gln

55

60

65

aag atc acc tcc tgg atg gag ccg ata gtc aag ttc ccg ggg gcc gtg 353

232/307

Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys Phe Pro Gly Ala Val
 70 75 80 85
 gac ggc gca acc tat atc ctg gtg atg gtg gat cca gat gcc cct agc 401
 Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser
 90 95 100
 aga gca gaa ccc aga cag aga ttc tgg aga cat tgg ctg gta aca gat 449
 Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp
 105 110 115
 atc aag ggc gcc gac ctg aag aaa ggg aag att cag ggc cag gag tta 497
 Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu
 120 125 130
 tca gcc tac cag gct ccc tcc cca ccg gca cac agt ggc ttc cat cgc 545
 Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg
 135 140 145
 tac cag ttc ttt gtc tat ctt cag gaa gga aaa gtc atc tct ctc ctt 593
 Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu
 150 155 160 165
 ccc aag gaa aac aaa act cga ggc tct tgg aaa atg gac aga ttt ctg 641
 Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe Leu
 170 175 180
 aac cgt ttc cac ctg ggc gaa cct gaa gca agc acc cag ttc atg acc 689
 Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe Met Thr
 185 190 195
 cag aac tac cag gac tca cca acc ctc cag gct ccc aga gaa agg gcc 737
 Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg Glu Arg Ala

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200 205 210
 agc gag ccc aag cac aaa aac cag gcg gag ata gct gcc tgc t 780
 Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile Ala Ala Cys

215 220 225
 agatagccgg ctttgccatc cgggcatgtg gccacactgc ccaccaccga cgatgtgggt 840
 atggaacccc ctctggatac agaaccctt cttttccaaa taataaaaaa atcatcc 897

<210> 115

<211> 1866

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (142)... (1467)

<400> 115

gcccgcagtc gggggcgtgg cagtcaacag caacaaccca cagcccgca gggccagaaa 60
 ctcccatctc cctcaccage cggaagtag gagtcggctc agcctggagg gacccaacca 120
 gagcctggcc tgggagccag g atg gcc atc cac aaa gcc ttg gtg atg tgc 171

Met Ala Ile His Lys Ala Leu Val Met Cys

1 5 10
 ctg gga ctg cct ctc ttc ctg ttc cca ggg gcc tgg gcc cag gcc cat 219
 Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala Gln Gly His

15 20 25
 gtc cca ccc ggc tgc agc caa ggc ctc aac ccc ctg tac tac aac ctg 267
 Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu

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30	35	40	
tgt gac cgc tct ggg gcg tgg ggc atc gtc ctg gag gcc gtg gct ggg			315
Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala Val Ala Gly			
45	50	55	
gcg ggc att gtc acc acg ttt gtg ctc acc atc atc ctg gtg gcc agc			363
Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu Val Ala Ser			
60	65	70	
ctc ccc ttt gtg cag gac acc aag aaa cgg agc ctg ctg ggg acc cag			411
Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln			
75	80	85	90
gta ttc ttc ctt ctg ggg acc ctg ggc ctc ttc tgc ctc gtg ttt gcc			459
Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu Val Phe Ala			
95	100	105	
tgt gtg gtg aag ccc gac ttc tcc acc tgt gcc tct cgg cgc ttc ctc			507
Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu			
110	115	120	
ttt ggg gtt ctg ttc gcc atc tgc ttc tct tgt ctg gcg gct cac gtc			555
Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala Ala His Val			
125	130	135	
ttt gcc ctc aac ttc ctg gcc cgg aag aac cac ggg ccc cgg ggc tgg			603
Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro Arg Gly Trp			
140	145	150	
gtg atc ttc act gtg gct ctg ctg ctg acc ctg gta gag gtc atc atc			651
Val Ile Phe Thr Val Ala Leu Leu Leu Thr Leu Val Glu Val Ile Ile			
155	160	165	170

235/307

aat aca gag tgg ctg atc atc acc ctg gtt cgg ggc agt ggc gag ggc	699
Asn Thr Glu Trp Leu Ile Ile Thr Leu Val Arg Gly Ser Gly Glu Gly	
175 180 185	
ggc cct cag ggc aac agc agc gca ggc tgg gcc gtg gcc tcc ccc tgt	747
Gly Pro Gln Gly Asn Ser Ser Ala Gly Trp Ala Val Ala Ser Pro Cys	
190 195 200	
gcc atc gcc aac atg gac ttt gtc atg gca ctc atc tac gtc atg ctg	795
Ala Ile Ala Asn Met Asp Phe Val Met Ala Leu Ile Tyr Val Met Leu	
205 210 215	
ctg ctg ctg ggt gcc ttc ctg ggg gcc tgg ccc gcc ctg tgt ggc cgc	843
Leu Leu Leu Gly Ala Phe Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg	
220 225 230	
tac aag cgc tgg cgt aag cat ggg gtc ttt gtg ctc ctc acc aca gcc	891
Tyr Lys Arg Trp Arg Lys His Gly Val Phe Val Leu Leu Thr Thr Ala	
235 240 245 250	
acc tcc gtt gcc ata tgg gtg gtg tgg atc gtc atg tat act tac ggc	939
Thr Ser Val Ala Ile Trp Val Val Trp Ile Val Met Tyr Thr Tyr Gly	
255 260 265	
aac aag cag cac aac agt ccc acc tgg gat gac ccc acg ctg gcc atc	987
Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile	
270 275 280	
gcc ctc gcc gcc aat gcc tgg gcc ttc gtc ctc ttc tac gtc atc ccc	1035
Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro	
285 290 295	
gag gtc tcc cag gtg acc aag tcc agc cca gag caa agc tac cag ggg	1083

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Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly
 300 305 310
 gac atg tac ccc acc cgg ggc gtg ggc tat gag acc atc ctg aaa gag 1131
 Asp Met Tyr Pro Thr Arg Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu
 315 320 325 330
 cag aag ggt cag agc atg ttc gtg gag aac aag gcc ttt tcc atg gat 1179
 Gln Lys Gly Gln Ser Met Phe Val Glu Asn Lys Ala Phe Ser Met Asp
 335 340 345
 gag ccg gtt gca gct aag agg ccg gtg tca cca tac agc ggg tac aat 1227
 Glu Pro Val Ala Ala Lys Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn
 350 355 360
 ggg cag ctg ctg acc agt gtg tac cag ccc act gag atg gcc ctg atg 1275
 Gly Gln Leu Leu Thr Ser Val Tyr Gln Pro Thr Glu Met Ala Leu Met
 365 370 375
 cac aaa gtt ccg tcc gaa gga gct tac gac atc atc ctc cca cgg gcc 1323
 His Lys Val Pro Ser Glu Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala
 380 385 390
 acc gcc aac agc cag gtg atg ggc agt gcc aac tcg acc ctg cgg gct 1371
 Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr Leu Arg Ala
 395 400 405 410
 gaa gac atg tac tcg gcc cag agc cac cag gcg gcc aca ccg ccg aaa 1419
 Glu Asp Met Tyr Ser Ala Gln Ser His Gln Ala Ala Thr Pro Pro Lys
 415 420 425
 gac ggc aag aac tct cag gtc ttt aga aac ccc tac gtg tgg gac 1464
 Asp Gly Lys Asn Ser Gln Val Phe Arg Asn Pro Tyr Val Trp Asp

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430	435	440	
tgagtc agcgggtggcg aggagaggcg gtcggatttg gggagggccc tgaggacctg			1520
gccccgggca agggactctc caggtcctc ctccccctgg caggcccagc aacatgtgcc			1580
ccagatgtgg aagggcctcc ctctctgcca gtgtttgggt ggggtgcatg ggtgtcccca			1640
cccactctc agtgtttgtg gagtcgagga gccaaccca gcctcctgcc aggatcacct			1700
cggcggtcac actccagcca aatagtgttc tcgggggtgt ggctgggcag cgcctatgtt			1760
tctctggaga ttctgcaac ctcaagagac ttcccaggcg ctccaggcctg gatcttctc			1820
ctctgtgagg aacaagggtg cctaataaat acatttctgc tttatt			1866

<210> 116

<211> 2198

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)... (847)

<400> 116

aaaatggcgt agagcctagc aacagcgcag gctcccagcc gagtccgtt atg gcc	55
---	----

Met Ala

1

gct gcc gtc ccg aag agg atg agg ggg cca gca caa gcg aaa ctg ctg	103
---	-----

Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys Leu Leu

5

10

15

ccc ggg tcg gcc atc caa gcc ctt gtg ggg ttg gcg cgg ccg ctg gtc	151
---	-----

Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro Leu Val

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20	25	30	
ttg gcg ctc ctg ctt gtg tcc gcc gct cta tcc agt gtt gta tca cgg			199
Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val Ser Arg			
35	40	45	50
act gat tca ccg agc cca acc gta ctc aac tca cat att tct acc cca			247
Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser Thr Pro			
	55	60	65
aat gtg aat gct tta aca cat gaa aac caa acc aaa cct tct att tcc			295
Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser Ile Ser			
	70	75	80
caa atc agc acc acc ctc cct ccc acg acg agt acc aag aaa agt gga			343
Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly			
	85	90	95
gga gca tct gtg gtc cct cat ccc tcg cct act cct ctg tct caa gag			391
Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser Gln Glu			
	100	105	110
gaa gct gat aac aat gaa gat cct agt ata gag gag gag gat ctt ctc			439
Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu			
	115	120	125
130			
atg ctg aac agt tct cca tcc aca gcc aaa gac act cta gac aat ggc			487
Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly			
	135	140	145
gat tat gga gaa cca gac tat gac tgg acc acg ggc ccc agg gac gac			535
Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp			
	150	155	160

239/307

gac gag tct gat gac acc ttg gaa gaa aac agg ggt tac atg gaa att	583
Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile	
165 170 175	
gaa cag tca gtg aaa tct ttt aag atg cca tcc tca aat ata gaa gag	631
Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile Glu Glu	
180 185 190	
gaa gac agc cat ttc ttt ttt cat ctt att att ttt gct ttt tgc att	679
Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe Cys Ile	
195 200 205 210	
gct gtt gtt tac att aca tat cac aac aaa agg aag att ttt ctt ctg	727
Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe Leu Leu	
215 220 225	
gtt caa agc agg aaa tgg cgt gat ggc ctt tgt tcc aaa aca gtg gaa	775
Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr Val Glu	
230 235 240	
tac cat cgc cta gat cag aat gtt aat gag gca atg cct tct ttg aag	823
Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser Leu Lys	
245 250 255	
att acc aat gat tat att ttt taaagc actgtgattt gaatttgctt	870
Ile Thr Asn Asp Tyr Ile Phe	
260 265	
atgtaatttt atttgcttga ctttttatat gatattgtgc aaatgtttgc cataggcaat	930
tggtacttaa atgagaggtg agtctctctt ttgccttggt gctttggaaa ttaaagtca	990
caaacgagta tataattttt tatctgtact tttagagctg agtttaatca ggtgtccaaa	1050
atgtgagtta aacattacct tatatttaca ctgtagttt ttattgtttt agatttatta	1110

240/307

tgcttcttct ggaagtatta gtgatgtac ttttaaaga tccaaactt gtaactaaat 1170
 tctgacatat ctgttactgc tgactcacat tcattctccg ccattcaaact actatTTTT 1230
 atccacattt tttttgttc ccaaactgta atgtacaagg atatgtgtga taatgcttg 1290
 gatttgagta atatTTTTt ttcttccaag aaaactgctt tggatattt tagataattt 1350
 aaacataatt taggataatg atattgtca atctgaccac aattttaggt aaaacattaa 1410
 atgtgtcaag aaatcttggc aacagagact ctgcagcttg cagtggacat agataaaatg 1470
 ttacagagat actatTTTTt tggttggaat tactatatta aatttagaag cagaaactgg 1530
 taaaatgta aatacatgta caattgctt tagtttagca ttgattgtag catgggttcc 1590
 tccaagggtt caagcaatgg gcagagtta aaattatc agattcggtt acttcgttta 1650
 ttattttaca gtaaattga ataaatctta ggggtcatta tcacttaaata aatactgtac 1710
 ctaggtctt caaattaaaa ttatacctga atgaagtgt ttgtatacat aaaggatatt 1770
 tgtgtacaat tacctTTTTt cccccacact tgtttctt gttttgtt tttatggcaa 1830
 ctggaaagta ttactatgg gattcattta tgtctgtctt tctatcataa agaattgatc 1890
 aatatgtaaa tatgtgattt gaaccatggt tgacttacaa gtgtcactac agcttttttag 1950
 aaaacatagc cctaatatat gttaagcagg acccggtga gccagtgggc ttgcgcttta 2010
 tgtagagctg gaagaaggcc gtccatcctg tctcttgggc ggacagtga ctttctaata 2070
 aggaaggga agcacaatgg aaataccct gaaccgtttt attgcagtaa ttttttcat 2130
 atctgaaact attatttaata atttgaata agatttttaa aaataaatgg caaagatata 2190
 aatctatg 2198

<210> 117

<211> 2180

<212> DNA

<213> Homo sapiens

<220>

241/307

<221> CDS

<222> (69)... (695)

<400> 117

aaccagcgcc gcggacaccg gcaccggcgc cacggactcc gcaggacccc gcgcccgcgc	60
ccgccgct atg ctg ggg ctg ctg gtg gcg ttg ctg gcc ctg ggg ctc gct	110
Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala	
1 5 10	
gtc ttt gcg ctg ctg gac gtc tgg tac ctg gtg cgc ctt ccg tgc gcc	158
Val Phe Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala	
15 20 25 30	
gtg ctg cgc gcg cgc ctg ctg cag ccg cgc gtc cgt gac ctg cta gct	206
Val Leu Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala	
35 40 45	
gag cag cgc ttc ccg ggc cgc gtg ctg ccc tcg gac ttg gac ctg ctg	254
Glu Gln Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu	
50 55 60	
ttg cac atg aac aac gcg cgc tac ctg cgc gag gcc gac ttt gcg cgc	302
Leu His Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg	
65 70 75	
gtc gcg cac ctg acc cgc tgc ggg gtg ctc ggg gcg ctg agg gag ttg	350
Val Ala His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu	
80 85 90	
cgg gcg cac acg gtg ctg gcg gcc tcg tgc gcg cgc cac cgc cgc tcg	398
Arg Ala His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser	
95 100 105 110	

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ctg cgc ctg ctg gag ccc ttc gag gtg cgc acc cgc ctg ctg ggc tgg	446
Leu Arg Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp	
115 120 125	
gac gac cgc gcg ttc tac ctg gag gcg cgc ttt gtc agc ctg cgg gac	494
Asp Asp Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp	
130 135 140	
ggt ttc gtg tgc gcg ctg ctg cgc ttc cgg cag cac ctg ctg ggc acc	542
Gly Phe Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr	
145 150 155	
tca ccc gag cgc gtc gtg cag cac ctg tgc cag cgc agg gtg gag ccc	590
Ser Pro Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro	
160 165 170	
cct gag ctg ccc gct gat ctg cag cac tgg atc tcc tac aac gag gcc	638
Pro Glu Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala	
175 180 185 190	
agc agc cag ctg ctc cgc atg gag agt ggg ctc agt gat gtc acc aag	686
Ser Ser Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys	
195 200 205	
gac cag tgaccgcc accttcacac cgtctgcct ggccaccatc ctgggcctgg	740
Asp Gln	
gggctgcca cagatgggca gtctcagcca tactctgttc cagctggagt agcctcctga	800
ccagcctggc ccacctgct ccaccactg ggcccccca gttattgata ccctctgtg	860
ctgggctcca cgctaggcag aaggaggagt ggcatgggca tctgaccca gctctgcct	920
caaggtgggg atggatgggc aaaggagagt cctgcctggc cctacgatga ggccactcat	980
gtgggcctag gtaggggagg atgggtgcctg gagcagaggg acccacaagt gcctcccgag	1040

243/307

cctagatcct ggctcggacc actgcaaggg ccgaggcagg gccagaccag agcatcctgg 1100
gtacaggcct gggctctcca gggcctgggc ctgattcagg tgcagtgggc actcctgaag 1160
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cacaggggct cctggaaaga cagcaggctt cctgctgggc gttcccttgt tggagggaat 1460
agagtggggg tgggactctg caggggtgtc cttgtccact cgcaccctc gcccccacc 1520
agggccatgc tctgtgactt gggtgatcc ccacccttc tgggcctaca gcaccacagg 1580
ccgctgtacc cccttagagc tgcccctctc tggcctggcc ggcagacgtc ttcttaactc 1640
ctctgtctc tatattcagc atgttccctg tcagctgctg ggccggccct gccttgcgt 1700
agcagagcct ctctggcag cttctcaggt ctccctaag gagacaccag gctactagga 1760
cactggctgg ggccaccccc tctgcctaa tgctcacct tacagctggg gaaactgagg 1820
cctggaatgg ccagagtca ccaaggcaaa gttggggctg gtcccagcct gaggctccag 1880
ctgatgcct cagctcccag agagggggtg ccccatctag ctgggtgcag gggtcactgc 1940
ttgtcagctc agggccctgt gcccgttgc ctgttccct acatctgtgc ctgcacatcc 2000
agaactgcct ccttgcgct gcctccagga agcccacct gagccagagt caagggtgc 2060
agcactgccc gatagaacac gcccgcctc actgtgttc ttgccttaca gccaccatgg 2120
gaaagctgca acctttctgt tttatttaa gaaagccaa cattaaaggg ttttcattgc 2180

<210> 118

<211> 1527

<212> DNA

<213> Homo sapiens

<220>

244/307

<221> CDS

<222> (103)... (1305)

<400> 118

agtccttcag ggcggcggtg ggtgtccgct tctctctgct ctgcgactgc accgcactcg 60

cgcgtgaccc tgactccccc tagtcagctc agcgggtgctg cc atg gcg tgg cgg 114

Met Ala Trp Arg

1

cgg cgc gaa gcc agc gtc ggg gct cgc ggc gtg ttg gct ctg gcg ttg 162

Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu Ala Leu Ala Leu

5 10 15 20

ctc gcc ctg gcc ctg tgc gtg ccc ggg gcc cgg ggc cgg gct ctc gag 210

Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly Arg Ala Leu Glu

25 30 35

tgg ttc tcg gcc gtg gta aac atc gag tac gtg gac ccg cag acc aac 258

Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp Pro Gln Thr Asn

40 45 50

ctg acg gtg tgg agc gtc tcg gag agt ggc cgc ttc ggc gac agc tcg 306

Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe Gly Asp Ser Ser

55 60 65

ccc aag gag ggc gcg cat ggc ctg gtg ggc gtc ccg tgg gcg ccc ggc 354

Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro Trp Ala Pro Gly

70 75 80

gga gac ctc gag ggc tgc gcg ccc gac acg cgc ttc ttc gtg ccc gag 402

Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe Phe Val Pro Glu

85 90 95 100

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ccc ggc ggc cga ggg gcc gcg ccc tgg gtc gcc ctg gtg gct cgt ggg	450
Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu Val Ala Arg Gly	
105 110 115	
ggc tgc acc ttc aag gac aag gtg ctg gtg gcg gcg cgg agg aac gcc	498
Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala Arg Arg Asn Ala	
120 125 130	
tcg gcc gtc gtc ctc tac aat gag gag cgc tac ggg aac atc acc ttg	546
Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly Asn Ile Thr Leu	
135 140 145	
ccc atg tct cac gcg gga aca gga aat ata gtg gtc att atg att agc	594
Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val Ile Met Ile Ser	
150 155 160	
tat cca aaa gga aga gaa att ttg gag ctg gtg caa aaa gga att cca	642
Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln Lys Gly Ile Pro	
165 170 175 180	
gta acg atg acc ata ggg gtt gcc acc cgg cat gta cag gag ttc atc	690
Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val Gln Glu Phe Ile	
185 190 195	
agc ggt cag tct gtg gtg ttt gtg gcc att gcc ttc atc acc atg atg	738
Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe Ile Thr Met Met	
200 205 210	
att atc tcg tta gcc tgg cta ata ttt tac tat ata cag cgt ttc cta	786
Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile Gln Arg Phe Leu	
215 220 225	
tat act ggc tct cag att gga agt cag agc cat aga aaa gaa act aag	834

246/307

Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg Lys Glu Thr Lys
 230 235 240
 aaa gtt att ggc cag ctt cta ctt cat act gta aag cat gga gaa aag 882
 Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys His Gly Glu Lys
 245 250 255 260
 gga att gat gtt gat gct gaa aat tgt gca gtg tgt att gaa aat ttc 930
 Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys Ile Glu Asn Phe
 265 270 275
 aaa gta aag gat att att aga att ctg cca tgc aag cat att ttt cat 978
 Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys His Ile Phe His
 280 285 290
 aga ata tgc att gac cca tgg ctt ttg gat cac cga aca tgt cca atg 1026
 Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg Thr Cys Pro Met
 295 300 305
 tgt aaa ctt gat gtc atc aaa gcc cta gga tat tgg gga gag cct ggg 1074
 Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp Gly Glu Pro Gly
 310 315 320
 gat gta cag gag atg cct gct cca gaa tct cct cct gga agg gat cca 1122
 Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro Gly Arg Asp Pro
 325 330 335 340
 gct gca aat ttg agt cta gct tta cca gat gat gac gga agt gat gag 1170
 Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp Gly Ser Asp Glu
 345 350 355
 agc agt cca cca tca gcc tcc cct gct gaa tct gag cca cag tgt gat 1218
 Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu Pro Gln Cys Asp

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360	365	370	
ccc agc ttt aaa gga gat gca gga gaa aat acg gca ttg cta gaa gcc	1266		
Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala Leu Leu Glu Ala			
375	380	385	
ggc agg agt gac tct cgg cat gga gga ccc atc tcc tagcacac	1310		
Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser			
390	395	400	
gtgcccactg aagtggcacc aacagaagtt tggcttgaac taaaggacat tttatttttt	1370		
ttacttttagc acataatttg tatatttgaa aataatgtat attattttac ctattagatt	1430		
ctgatttgat atacaaagga ctaagatatt ttcttcttga agagactttt cgattagtcc	1490		
tcatatattt atctactaaa atagagtgtt taccatg	1527		

<210> 119

<211> 1905

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125)... (703)

<400> 119

gagcctaacc tagagtgctc gcagcagtct ttcagttgag cttggggact gcagctgtgg	60
ggagatttca gtgcattgcc tcccctgggt gctcttcac ttggatttga aagttgagag	120
cagc atg ttt tgc cca ctg aaa ctc atc ctg ctg cca gtg tta ctg gat	169
Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp	

1

5

10

15

248/307

tat tcc ttg ggc ctg aat gac ttg aat gtt tcc ccg cct gag cta aca	217
Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr	
20 25 30	
gtc cat gtg ggt gat tca gct ctg atg gga tgt gtt ttc cag agc aca	265
Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr	
35 40 45	
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag	313
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu	
50 55 60	
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg	361
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val	
65 70 75	
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac aac tta	409
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu	
80 85 90 95	
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag	457
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln	
100 105 110	
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc	505
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe	
115 120 125	
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa gag ctc	553
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu	
130 135 140	
atg gtc cat gtg ggt gga ttg att cag atg gga tgt gtt ttc cag agc	601

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Met Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser

145 150 155

aca gaa gtg aaa cac gtg acc aag gta gaa tgg ata ttt tca gga cgg 649

Thr Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg

160 165 170 175

cgc gca aag gta aca agg agg aaa cat cac tgt gtt aga gaa ggc tct 697

Arg Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser

180 185 190

ggc tgatggtatc aggacaaagg tagaatcagg cacatgagga ggtgttgcaa 750

Gly

gagcctgggc tttggtgctt atcagaactg gaccttctcc tagcaatttc agctttctgg 810

tgggaaagat aactccaatg aagaacaaga acaagaagat gatgatgatg cttaactttt 870

tggatgccga tatgagattg tacatgagga gattgtattt cgttactacc acaaactcag 930

gatgtctgcg gagtactccc agagctgggg ccacttcag aatcgtgtga acctggtggg 990

ggacattttc cgcaatgacg gttccatcat gttcaagga gtgagggagt cagatggagg 1050

aaactacacc tgcagtatcc acctagggaa cctgggtgtc aagaaaacca ttgtgctgca 1110

tgtcagcccg gaagagcctc gaacactggt gaccccgga gccctgaggc ctctggtctt 1170

gggtggtaat cagtgtgtga tcattgtggg aattgtctgt gccacaatcc tgetgctccc 1230

tgttctgata ttgatcgtga agaagacctg tggaaataag agttcagtga attctacagt 1290

cttggtgaag aacacgaaga agactaatcc agagataaaa gaaaaaccct gccattttga 1350

aagatgtgaa ggggagaaac acatttactc cccaataatt gtacgggagg tgatcgagga 1410

agaagaacca agtgaaaaat cagaggccac ctacatgacc atgcacccag tttggccttc 1470

tctgaggtca gatcgaaca actcacttga aaaaaagtca ggtgggggaa tgccaaaaac 1530

acagcaagcc ttttgagaag aatggagagt ccttcatct cagcagcggg ggagactctc 1590

tcctgtgtgt gtccctgggac actctaccag tgatttcaga ctcccgtctt cccagctgtc 1650

250/307

ctcctgtctc attgtttggt caatacactg aagatggaga atttgagacc tggcagagag 1710
 actggacagc tctggaggaa caggcctgct gagggagagg gagcatggac ttggcctctg 1770
 gagtgggaca ctggccctgg gaaccaggct gagctgagtg gcctcaaacc ccccgttgga 1830
 tcagaccctc ctgtgggcag ggttcttagt ggatgagtta ctgggaagaa tcagagataa 1890
 aaaccaaccc aaatc 1905

<210> 120

<211> 998

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)... (832)

<400> 120

gcacttgcca gccagtcgc ccgccggag cccggctcgc tggggcagc atg gcg 55

Met Ala

1

ggg tcg ccg ctg ctc tgg ggg ccg cgg gcc ggg ggc gtc ggc ctt ttg 103

Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly Leu Leu

5

10

15

gtg ctg ctg ctg ctc ggc ctg ttt cgg ccg ccc ccc gcg ctc tgc gcg 151

Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu Cys Ala

20

25

30

cgg ccg gta aag gag ccc cgc ggc cta agc gca gcg tct ccg ccc ttg 199

Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro Pro Leu

251/307

35	40	45	50	
gct gag act ggc gct cct cgc cgc ttc cgg cgg tca gtg ccc cga ggt				247
Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro Arg Gly				
	55	60	65	
gag gcg gcg ggg gcg gtg cag gag ctg gcg cgg gcg ctg gcg cat ctg				295
Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu				
	70	75	80	
ctg gag gcc gaa cgt cag gag cgg gcg cgg gcc gag gcg cag gag gct				343
Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala				
	85	90	95	
gag gat cag cag gcg cgc gtc ctg gcg cag ctg ctg cgc gtc tgg ggc				391
Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val Trp Gly				
100	105	110		
gcc ccc cgc aac tct gat ccg gct ctg ggc ctg gac gac gac ccc gac				439
Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp Pro Asp				
115	120	125	130	
gcg cct gca gcg cag ctc gct cgc gct ctg ctc cgc gcc cgc ctt gac				487
Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp				
	135	140	145	
cct gcc gcc ctc gca gcc cag ctt gtc ccc gcg ccc gtc ccc gcc gcg				535
Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro Ala Ala				
	150	155	160	
gcg ctc cga ccc cgg ccc ccg gtc tac gac gac ggc ccc gcg ggc ccg				583
Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala Gly Pro				
165	170	175		

252/307

gat gct gag gag gca ggc gac gag aca ccc gac gtg gac ccc gag ctg	631
Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro Glu Leu	
180 185 190	
ttg agg tac ttg ctg gga cgg att ctt gcg gga agc gcg gac tcc gag	679
Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp Ser Glu	
195 200 205 210	
ggg gtg gca gcc ccg cgc cgc ctc cgc cgt gcc gcc gac cac gat gtg	727
Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His Asp Val	
215 220 225	
ggc tct gag ctg ccc cct gag ggc gtg ctg ggg gcg ctg ctg cgt gtg	775
Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu Arg Val	
230 235 240	
aaa cgc cta gag acc ccg gcg ccc cag gtg cct gca cgc cgc ctc ttg	823
Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg Leu Leu	
245 250 255	
cca ccc t gagcactgcc cggatcccggt gcaccctggg acccagaagt gcccccgcca	880
Pro Pro	
260	
tcccgccacc aggactgctc cccgccagca cgtccagagc aacttacccc ggccagccag	940
ccctctcacc cgaggatccc taccctctgg ccccaata aacatgatct gaagcagc	998

<210> 121

<211> 337

<212> PRT

<213> Homo sapiens

253/307

<400> 121

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly Ala Gly Gly Glu Pro

1 5 10 15

Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg Leu Leu Ser Ala Leu

20 25 30

Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu Val Asn Lys Ala Leu

35 40 45

Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe Leu Gly Ile Gly Gln

50 55 60

Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser Lys Leu Asn Lys Ile

65 70 75 80

Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro Val Lys Leu Phe Pro

85 90 95

Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser Gly Leu Ser Ser Thr

100 105 110

Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu Arg Lys Phe Thr Ile

115 120 125

Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu Gly Lys Gln Tyr Ser

130 135 140

Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile Leu Gly Ala Phe Ile

145 150 155 160

Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu Gly Tyr Ile Phe Val

165 170 175

Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly Val Tyr Thr Lys Gln

180 185 190

254/307

Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly Val Leu Phe Tyr Asn

195

200

205

Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile Ser Val Ser Thr Gly

210

215

220

Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp Lys Asn Val Val Phe

225

230

235

240

Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly Phe Leu Leu Met Tyr

245

250

255

Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala Leu Thr Thr Ala Val

260

265

270

Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr Ile Gly Ile Leu Ile

275

280

285

Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe Val Gly Leu Asn Ile

290

295

300

Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu Thr Leu Ser Ser Gln

305

310

315

320

Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile Cys Leu Asp Leu Lys

325

330

335

Ser

<210> 122

<211> 236

<212> PRT

<213> Homo sapiens

255/307

<400> 122

Met Ala Glu Ala Glu Glu Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro
 1 5 10 15
 Arg Pro Leu Phe Ala Gly Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile
 20 25 30
 Pro Val Glu Gly Glu Ile Thr Ile Pro Met Arg Ser Arg Ile Arg Glu
 35 40 45
 Phe Asp Ser Ser Thr Leu Asn Glu Ser Val Arg Asn Thr Ile Met Arg
 50 55 60
 Asp Leu Lys Ala Val Gly Lys Lys Phe Met His Val Leu Tyr Pro Arg
 65 70 75 80
 Lys Ser Asn Thr Leu Leu Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile
 85 90 95
 Leu Cys Val Thr Leu Ala Leu Met Leu Gln Arg Asp Ser Ala Asp Ser
 100 105 110
 Glu Lys Asp Gly Gly Pro Gln Phe Ala Glu Val Phe Val Ile Val Trp
 115 120 125
 Phe Gly Ala Val Thr Ile Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn
 130 135 140
 Ile Ser Phe Phe Gln Ser Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro
 145 150 155 160
 Leu Thr Val Ala Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro
 165 170 175
 Gly Pro Val Asn Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe
 180 185 190

256/307

Ala Trp Ser Ile Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro

195

200

205

Pro Asn Arg Arg Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe

210

215

220

Val Ile Ser Trp Met Ile Leu Thr Phe Thr Pro Gln

225

230

235

<210> 123

<211> 560

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg Arg Lys Thr Gly Tyr Ser

1

5

10

15

Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro Gly Arg Gly Pro Ala Gly

20

25

30

Ser Pro Ala His Leu His Thr Gly Thr Phe Trp Leu Thr Arg Ile Val

35

40

45

Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe Val Ala Phe Leu Val Ala

50

55

60

Phe His Gln Asn Lys Gln Leu Ile Gly Asp Arg Gly Leu Leu Pro Cys

65

70

75

80

Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr Phe Gln Asp Arg Thr Ser

85

90

95

Trp Glu Val Phe Ser Tyr Met Pro Thr Ile Leu Trp Leu Met Asp Trp

257/307

100	105	110	
Ser Asp Met Asn Ser Asn Leu Asp Leu Leu Ala Leu Leu Gly Leu Gly			
115	120	125	
Ile Ser Ser Phe Val Leu Ile Thr Gly Cys Ala Asn Met Leu Leu Met			
130	135	140	
Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu Val Asn Val Gly His Val			
145	150	155	160
Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu Leu Glu Thr Gly Phe Leu			
165	170	175	
Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu Ser Arg Leu Pro Gln His			
180	185	190	
Thr Pro Thr Ser Arg Ile Val Leu Trp Gly Phe Arg Trp Leu Ile Phe			
195	200	205	
Arg Ile Met Leu Gly Ala Gly Leu Ile Lys Ile Arg Gly Asp Arg Cys			
210	215	220	
Trp Arg Asp Leu Thr Cys Met Asp Phe His Tyr Glu Thr Gln Pro Met			
225	230	235	240
Pro Asn Pro Val Ala Tyr Tyr Leu His His Ser Pro Trp Trp Phe His			
245	250	255	
Arg Phe Glu Thr Leu Ser Asn His Phe Ile Glu Leu Leu Val Pro Phe			
260	265	270	
Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile Ile His Gly Val Leu Gln			
275	280	285	
Ile Leu Phe Gln Ala Val Leu Ile Val Ser Gly Asn Leu Ser Phe Leu			
290	295	300	

258/307

Asn Trp Leu Thr Met Val Pro Ser Leu Ala Cys Phe Asp Asp Ala Thr
305 310 315 320
Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly Ser Leu Lys Asp Arg Val
325 330 335
Leu Gln Met Gln Arg Asp Ile Arg Gly Ala Arg Pro Glu Pro Arg Phe
340 345 350
Gly Ser Val Val Arg Arg Ala Ala Asn Val Ser Leu Gly Val Leu Leu
355 360 365
Ala Trp Leu Ser Val Pro Val Val Leu Asn Leu Leu Ser Ser Arg Gln
370 375 380
Val Met Asn Thr His Phe Asn Ser Leu His Ile Val Asn Thr Tyr Gly
385 390 395 400
Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala Glu Val Ile Leu Gln Gly
405 410 415
Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp Ala Met Trp Glu Asp Tyr
420 425 430
Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser Arg Arg Pro Cys Leu Ile
435 440 445
Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu Met Trp Phe Ala Ala Phe
450 455 460
Gln Thr Tyr Glu His Asn Asp Trp Ile Ile His Leu Ala Gly Lys Leu
465 470 475 480
Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu Leu Ala His Asn Pro Phe
485 490 495
Ala Gly Arg Pro Pro Pro Arg Trp Val Arg Gly Glu His Tyr Arg Tyr

259/307

500 505 510
Lys Phe Ser Arg Pro Gly Gly Arg His Ala Ala Glu Gly Lys Trp Trp
515 520 525
Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro Pro Leu Ser Leu Glu Glu
530 535 540
Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp Pro Leu Pro Gly Pro Leu
545 550 555 560

<210> 124

<211> 406

<212> PRT

<213> Homo sapiens

<400> 124

Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn
1 5 10 15
Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu
20 25 30
Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg
35 40 45
Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile
50 55 60
Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val
65 70 75 80
Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu
85 90 95

260/307

Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu

100

105

110

Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly

115

120

125

Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser

130

135

140

Val Thr Leu Ala Ala Tyr Glu-Gys Asn Ser Val Asn Phe Pro Glu Pro

145

150

155

160

Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly

165

170

175

Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys

180

185

190

Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met

195

200

205

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr

210

215

220

Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe

225

230

235

240

Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly

245

250

255

Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp

260

265

270

Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe

275

280

285

Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln

261/307

290 295 300
 Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met
 305 310 315 320
 Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys
 325 330 335
 Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys
 340 345 350
 Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe
 355 360 365
 Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile
 370 375 380
 Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn
 385 390 395 400
 Ser Glu Glu Lys Thr Lys
 405

<210> 125

<211> 453

<212> PRT

<213> Homo sapiens

<400> 125

Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala Leu
 1 5 10 15
 Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe Asp Val
 20 25 30

262/307

Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly Gly Ala Val

35

40

45

Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val Gln Glu Gly His

50

55

60

Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly Glu Leu Val Leu Ala

65

70

75

80

Ser Gly Ala Gly Phe Gly Val Ser Asp Val Gly Ser His Leu Asp Cys

85

90

95

Gly Ala Gly Glu Pro Ala Val Phe Arg Asp Ser Asp Arg Phe Ser Trp

100

105

110

His Asp Pro His Leu Trp Arg Ser Gly Asp Glu Ala Pro Gly Leu Phe

115

120

125

Phe Val Asp Ala Glu Arg Val Pro Cys Arg His Asp Asp Val Phe Phe

130

135

140

Pro Pro Ser Ala Ser Phe Arg Val Gly Leu Gly Pro Gly Ala Ser Pro

145

150

155

160

Val Arg Val Arg Ser Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp

165

170

175

Glu Asp Leu Ala Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe

180

185

190

His Gly Pro Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro

195

200

205

Ser Gly Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala

210

215

220

Ala Leu Leu Gln Pro Leu Gly Gly Arg Cys Pro Gln Ala Ala Cys His

263/307

225 230 235 240
Ser Ala Leu Arg Pro Gln Gly Gln Cys Cys Asp Leu Cys Gly Ala Val
245 250 255
Val Leu Leu Thr His Gly Pro Ala Phe Asp Leu Glu Arg Tyr Arg Ala
260 265 270
Arg Ile Leu Asp Thr Phe Leu Gly Leu Pro Gln Tyr His Gly Leu Gln
275 280 285
Val Ala Val Ser Lys Val Pro Arg Ser Ser Arg Leu Arg Glu Ala Asp
290 295 300
Thr Glu Ile Gln Val Val Leu Val Glu Asn Gly Pro Glu Thr Gly Gly
305 310 315 320
Ala Gly Arg Leu Ala Arg Ala Leu Leu Ala Asp Val Ala Glu Asn Gly
325 330 335
Glu Ala Leu Gly Val Leu Glu Ala Thr Met Arg Glu Ser Gly Ala His
340 345 350
Val Trp Gly Ser Ser Ala Ala Gly Leu Ala Gly Gly Val Ala Ala Ala
355 360 365
Val Leu Leu Ala Leu Leu Val Leu Leu Val Ala Pro Pro Leu Leu Arg
370 375 380
Arg Ala Gly Arg Leu Arg Trp Arg Arg His Glu Ala Ala Ala Pro Ala
385 390 395 400
Gly Ala Pro Leu Gly Phe Arg Asn Pro Val Phe Asp Val Thr Ala Ser
405 410 415
Glu Glu Leu Pro Leu Pro Arg Arg Leu Ser Leu Val Pro Lys Ala Ala
420 425 430

264/307

Ala Asp Ser Thr Ser His Ser Tyr Phe Val Asn Pro Leu Phe Ala Gly

435

440

445

Ala Glu Ala Glu Ala

450

<210> 126

<211> 59

<212> PRT

<213> Homo sapiens

<400> 126

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu

1

5

10

15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

20

25

30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu

35

40

45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met

50

55

<210> 127

<211> 210

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu

265/307

1	5	10	15
Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr			
20	25	30	
Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly			
35	40	45	
Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro			
50	55	60	
Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu			
65	70	75	80
Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro			
85	90	95	
Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr			
100	105	110	
Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp			
115	120	125	
Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro			
130	135	140	
Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly			
145	150	155	160
Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser			
165	170	175	
Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr			
180	185	190	
Pro Ser Ala Thr Arg Ser Cys Ser Gly Leu Val Gln Thr Ala Arg Gly			
195	200	205	

266/307

Gly Ser

210

<210> 128

<211> 165

<212> PRT

<213> Homo sapiens

<400> 128

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg Arg Arg Phe Leu Leu

1 5 10 15

Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu Gly Asp Ala Gly Pro

20 25 30

Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys Pro Leu Pro Arg Leu

35 40 45

Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser Ile Val Val Thr Tyr

50 55 60

Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn Phe His Thr Ser Ser

65 70 75 80

Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val Ser Leu Ser Ile Ala

85 90 95

Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys Gly Ile Gly Glu Tyr

100 105 110

Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr Thr Ala Ser Phe Ile

115 120 125

Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp His Val Trp Ser Phe

267/307

130 135 140
 Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met Gly Val Val Met Phe
 145 150 155 160
 Ile Thr Leu Leu Gly
 165

<210> 129

<211> 162

<212> PRT

<213> Homo sapiens

<400> 129

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
 1 5 10 15
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
 20 25 30
 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
 35 40 45
 Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
 50 55 60
 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
 65 70 75 80
 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
 85 90 95
 Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
 100 105 110

268/307

Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
115 120 125
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
130 135 140
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
145 150 155 160
Arg Arg

<210> 130

<211> 221

<212> PRT

<213> Homo sapiens

<400> 130

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly
1 5 10 15
Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu
20 25 30
Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu
35 40 45
Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
50 55 60
Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
65 70 75 80
Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
85 90 95

269/307

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100

105

110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe

115

120

125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145

150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

165

170

175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

180

185

190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

210

215

220

<210> 131

<211> 1011

<212> DNA

<213> Homo sapiens

<400> 131

atgacggccg gcggccaggc cgaggccgag ggcgctggcg gggagcccgg cgcggcgcgg 60

ctgccctcgc gggtagcccg gctgctgtcg gcgtcttct acgggacctg ctcttctctc 120

atcgtgcttg tcaacaaggc gctgctgacc acctacggtt tcccgtcacc aattttcctt 180

270/307

ggaattggac agatggcagc caccataatg atactatatg tgtccaagct aaacaaaatc 240
 attcacttcc ctgattttga taagaaaatt cctgtaaage tgtttcctct gcctctcctc 300
 tacgttggaa accacataag tggattatca agcacaagta aattaagcct accgatgttc 360
 accgtgctca ggaaattcac cattccactt accttacttc tggaaacat cataacttggg 420
 aagcagtatt cactcaacat catcctcagt gtctttgcc a ttattctcgg ggctttcata 480
 gcagctgggt ctgaccttgc ttttaactta gaaggctata tttttgtatt cctgaatgat 540
 atcttcacag cagcaaattg agtttatacc aaacagaaaa tggacccaaa ggagctaggg 600
 aaatacggag tacttttcta caatgcctgc ttcattgatta tcccaactct tattattagt 660
 gtctccactg gagacctgca acaggctact gaattcaacc aatggaagaa tgttgtgttt 720
 atcctacagt ttcttcttct ctgttttttg gggtttctgc tgatgtactc cacggttctg 780
 tgcagctatt acaattcagc cctgacgaca gcagtgggtg gagccatcaa gaatgtatcc 840
 gttgcctaca ttgggatatt aatcggtgga gactacattt tctctttgtt aaactttgta 900
 gggttaaata ttgcatggc agggggcctg agatattcct ttttaacact gacgagccag 960
 ttaaaaccta aacctgtggg tgaagaaaac atctgtttgg atttgaagag c 1011

<210> 132

<211> 708

<212> DNA

<213> Homo sapiens

<400> 132

atggcgggaag cggaggagtc tccaggagac ccggggacag catcgcccag gccctgttt 60
 gcaggccttt cagatatatc catctcacia gacatccccg tagaaggaga aatcaccatt 120
 cctatgagat ctgcacatcg ggagtttgac agctccacat taaatgaatc tgttcgcaat 180
 accatcatgc gtgatctaaa agctgttggg aaaaaattca tgcattgttt gtaccaagg 240
 aaaagtaata ctcttttgag agattgggat ttgtggggcc ctttgatcct ttgtgtgaca 300

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ctcgcatataa tgctgcaaag agactctgca gatagtgaag aagatggagg gcccgaattt 360
gcagagggtgt ttgtcattgt ctggtttggg gcagttacca tcacctcaa ctcaaaactt 420
cttggaggga acatatcttt ttttcagagc ctctgtgtgc tgggttactg tatacttccc 480
ttgacagtag caatgctgat ttgccggctg gtacttttgg ctgatccagg acctgtaaac 540
ttcatgggtc ggctttttgt ggtgattgtg atgtttgcct ggtctatagt tgcctccaca 600
gctttccttg ctgatagcca gcctccaaac cgcagagccc tagctgttta tctgttttc 660
ctgttttact ttgtcatcag ttggatgatt ctacacctta ctctcag 708

<210> 133

<211> 1680

<212> DNA

<213> Homo sapiens

<400> 133

atggcgggcg cgcgggagtc gctgaggagg cggaagactg ggtactcgga tccggagcct 60
gagtcgccgc ccgcgccggg gcgtggcccc gcaggctctc cggcccatct ccacacgggc 120
accttctggc tgaccgggat cgtgtctctg aaggccctag ccttcgtgta cttcgtggca 180
ttctgggtgg ctttccatca gaacaagcag ctcatcggtg acagggggct gcttccctgc 240
agagtgttcc tgaagaactt ccagcagtac ttccaggaca ggacgagctg ggaagtctc 300
agctacatgc ccaccatcct ctggctgatg gactggtcag acatgaactc caacctggac 360
ttgttggtc ttctcggact gggcatctcg tctttcgtac tgatcacggg ctgcgccaac 420
atgcttctca tggctgccct gtggggcctc tacatgtccc tggttaatgt gggccatgtc 480
tggtactctt tcggatggga gtcccagctt ctggagacgg ggttcttggg gatcttcctg 540
tgccctctgt ggacgtgtc aaggctgccc cagcataccc ccacatccc gattgtcctg 600
tggggcttcc ggtggctgat cttcaggatc atgcttggag caggcctgat caagatccgg 660
ggggaccggt gctggcgaga cctcacctgc atggacttcc actatgagac ccagccgatg 720

272/307

cccaatcctg tggcatacta cctgcaccac tcaccctggt ggttccatcg cttcgagacg 780
 ctcagcaacc acttcacga gctcctggcg cccttcttcc tcttctcgg ccggcggcg 840
 tgcacatcc acggggtgct gcagatcctg ttccaggccg tctcatcgt cagcgggaac 900
 ctcagcttcc tgaactggct gactatggcg ccagcctgg cctgcttga tgacgccacc 960
 ctgggattct tgttccctc tgggccaggc agcctgaagg accgagttct gcagatgcag 1020
 agggacatcc gaggggcccg gcccgagccc agattcggct ccgtggcg gcgtgcagcc 1080
 aacgtctcgc tgggcgtcct gctggcctgg ctcagcgtgc ccgtggctc caacttgctg 1140
 agctccaggc aggtcatgaa caccacttc aactctctc acatcgtcaa cacttacggg 1200
 gccttcggaa gcacaccaa ggagcggcg gaggtgatcc tgcaggcac agccagctcc 1260
 aacgccagcg ccccgatgc catgtgggag gactacgagt tcaagtcaa gccaggtgac 1320
 cccagcagac ggccctgcct catctcccc taccactacc gcctggactg gctgatgtgg 1380
 ttgcggcct tccagaccta cgagcacaac gactggatca tccacctggc tggcaagctc 1440
 ctggccagcg acgccaggc cttgtccctg ctggcacaca accccttcgc gggcaggccc 1500
 ccgccaggt gggtcgagg agagcactac aggtacaagt tcagccgtcc tgggggcagg 1560
 cacgcccg agggcaagt gtgggtgcgg aagaggatcg gacctaact cctccgctc 1620
 agcctggagg agctgagggc ctacttcagg gaccgtgggt ggccctctgc cgggcccctc 1680

<210> 134

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 134

atggcagaga atggaaaaa ttgtgaccag agacgtgtag caatgaacaa ggaacatcat 60
 aatggaaatt tcacagacc ctcttcagt aatgaaaaga agaggaggga gcgggaagaa 120
 aggcagaata ttgtcctgtg gagacagccg ctattacct tgcagtattt ttctctggaa 180

273/307

atccttgtaa tcttgaagga atggacctca aaattatggc atcgtcaaag catttgtgtg 240
 tcttttttac tgctgcttgc tgtgcttata gctacgtatt atgttgaagg agtgcacaa 300
 cagtatgtgc aacgtataga gaaacagttt cttttgtatg cctactggat aggcttagga 360
 attttgtctt ctgttgggct tggaacaggg ctgcacacct tctgcttta tctgggtcca 420
 catatagcct cagttacatt agctgcttat gaatgcaatt cagttaattt tcccgaacca 480
 ccctatcctg atcagattat ttgtccagat gaagagggca ctgaaggac catttcttg 540
 tggagtatca tctcaaaagt taggattgaa gcctgcatgt ggggtatcgg tacagcaatc 600
 ggagagctgc ctccatattt catggccaga gcagctgcc tctcaggtgc tgaaccagat 660
 gatgaagagt atcaggaatt tgaagagatg ctggaacatg cagagtctgc acaagacttt 720
 gcctcccggt ccaaactggc agttcaaaaa ctagtacaga aagtgggatt ttttgaatt 780
 ttggcctgtg cttcaattcc aaatccttta ttgatctgg ctggaataac gtgtggacac 840
 tttctggtac ctttttgac cttctttggt gcaaccctaa ttggaaaagc aataataaaa 900
 atgcataatc agaaaatttt tgttataata acattcagca agcacatagt ggagcaaagt 960
 gtggctttca ttggtgctgt ccccggcata ggtccatctc tgcagaagcc atttcaggag 1020
 tacctggagg ctcaacggca gaagcttcac cacaaaagcg aaatgggcac accacagggg 1080
 gaaaactggt tgtcctggat gtttgaagag ttggtcgttg tcatggtgtg ttacttcac 1140
 ctatctatca ttaactccat ggcacaaaagt tatgcaaac gaatccagca gcggttgaac 1200
 tcagaggaga aaactaaa 1218

<210> 135

<211> 1359

<212> DNA

<213> Homo sapiens

<400> 135

atgggcgtcc tgggcccgggt cctgctgtgg ctgcagctct gcgcactgac ccaggcggtc 60

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tccaaactct gggccccaa cacgacttc gacgtcgag ccaactggag ccagaaccgg 120
accccggtgcg ccggcggcgc cgttgagttc ccggcggaca agatggtgtc agtcctggtg 180
caagaaggtc acgccgtctc agacatgctc ctgccgttg atggggaact cgtcctggct 240
tcaggagccg gattcggcgt ctcagacgtg ggctcgcacc tggactgttg cgcgggcgaa 300
cctgccgtct tccgcgactc tgaccgcttc tcctggcatg acccgcacct gtggcgctct 360
ggggacgagg cacctggcct cttcttcgtg gacgccgagc gcgtgccctg ccgccacgac 420
gacgtcttct ttccgcctag tgcctccttc cgcgtggggc tcggcccttg cgctagcccc 480
gtgcgtgtcc gcagcatctc ggctctgggc cggacgttca cgcgcgacga ggacctggct 540
gttttcttg cgtcccgccg gggccgccta cgcttcacg ggccgggcgc gctgagcgtg 600
ggccccgagg actgcgcgga cccgtcgggc tgcgtctgcg gcaacgcgga ggcgagccg 660
tggatctgcg cgccctgct ccagcccctg ggccggcgt gccccaggc cgcctgccac 720
agcgccttc ggccccaggg gcagtgtgt gacctctgtg gagccgttgt gttgtgacc 780
cacggccccg catttgacct ggagcggtag cgggcgcgga tactggacac cttctgggt 840
ctgcctcagt accacgggct gcaggtggcc gtgtccaagg tgccacgtc gtcccggctc 900
cgtgaggccg atacggagat ccaggtggtg ctggtggaga atgggcccga gacaggcgga 960
gcggggcggc tggcccgggc cctcctggcg gacgtcgccg agaacggcga ggccctcggc 1020
gtcctggagg cgaccatgcg ggagtcgggc gcacacgtc tgggcagctc cgcggctggg 1080
ctggcgggcg gcgtggcggc tgccgtgtg ctggcgtgc tggtcctgct ggtggcgccg 1140
ccgctgtgc gccgcgcggg gaggtcagg tggaggaggc acgaggcggc ggccccggct 1200
ggagcgcgcc tcggcttcg caaccgggtg ttcgacgtga cggcctccga ggagctgccc 1260
ctgccgcggc ggctcagcct ggtccgaag gcggccgag acagcaccag ccacagttac 1320
ttcgtcaacc ctctgttcg cggggccgag gccgaggcc 1359

<210> 136

<211> 177

275/307

<212> DNA

<213> Homo sapiens

<400> 136

atgacctcag tttcaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct	60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc	120
attacaggca tttgtgcctg cttgggggta tatgcacgaa aaagaaatgg acagatg	177
atgacctcag tttcaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct	60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc	120
attacaggca tttgtgcctg cttgggggta tatgcacgaa aaagaaatgg acagatg	177

<210> 137

<211> 630

<212> DNA

<213> Homo sapiens

<400> 137

atggccctgc cccagatgtg tgacgggagc cacttggcct ccacctccg ctattgcatg	60
acagtcagcg gcacagtggg tctgggtggc gggacgctct gcttcgcttg gtggagcgaa	120
ggggatgcaa ccgccagcc tggccagctg gccccacca cggagtatcc ggtgcctgag	180
ggccccagcc cctgtctcag gtccgtcagc ttcgtctgct gcggtgcagg tggcctgctg	240
ctgtctattg gcctgtcttg gtccgtcaag gccagcatcc cagggccacc tcgatgggac	300
ccctatcacc tctccagaga cctgtactac ctactgtgg agtcctcaga gaaggagagc	360
tgcaggaccc ccaaagtggg tgacatcccc acttacgagg aagccgtgag cttcccagtg	420
gccgaggggc ccccaacacc acctgcatac cctacggagg aagccctgga gccaaagtga	480
tcgagggatg cctgtctcag caccagccc gcctggcctc caccagcta tgagagcatc	540
agccttgctc ttgatgccgt ttctgcagag acgacaccga gtgccacag ctctctgtca	600

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ggcctgggtc agactgcacg gggaggaagt

630

<210> 138

<211> 495

<212> DNA

<213> Homo sapiens

<400> 138

atggactcct cgcgggcccg acagcagctc cggcggcgat tcctcctcct gccggacgcc 60
gaggcccagc tggaccgcga gggtagcgcc gggccggaaa cctccacagc tgttgagaaa 120
aaggagaaac ctctccaag acttaataac cattctggat tctggatttt ggcatccatt 180
gttgtgacct attatgttga cttctttaaa acccttaaag aaaacttcca cactagcagc 240
tggtttctct gtggcagtgc cttgttgctt gtcagtttat caattgcatt ttactgcata 300
gtctacctgg aatggtattg tggaattgga gaatatgatg tcaagtatcc agccttgata 360
cccattacca ctgcctcctt tattgcagca ggaatttgct tcaacattgc tttatggcat 420
gtgtggtcgt ttttcactcc attgttggtg tttaccagct ttatgggggt tgcattgttt 480
atcacactcc ttgga 495

<210> 139

<211> 486

<212> DNA

<213> Homo sapiens

<400> 139

atgciccaga ccagtaacta cagcctgggtg ctctctctgc agttcctgct gctgtcctat 60
gacctctttg tcaattcctt ctcaaacctg ctccaaaaga ctctgtcat ccagcttggt 120
ctcttcatca tccaggatat tgcagtcctc ttcaacatca tcatcatttt cctcatgttc 180

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ttcaacacct tegtcttcca ggctggcctg gtcaacctcc tattccataa gttcaaaggg	240
accatcatcc tgacagctgt gtactttgcc ctacagcatct cccttcatgt ctgggtcatg	300
aacttacgct ggaaaaactc caacagcttc atatggacag atggacttca aatgctgttt	360
gtattccaga gactagcagc agtgtgttac tgctacttct ataaacggac agccgtaaga	420
ctaggcgatc ctcaattcta ccaggactct ttgtggctgc gcaaggagtt catgcaagtt	480
cgaagg	486

<210> 140

<211> 663

<212> DNA

<213> Homo sapiens

<400> 140

atggcgttgg cgttggcggc gctggcggcg gtcgagccgg cctgcggcag ccggtaccag	60
cagttgcaga atgaagaaga gtctggagaa cctgaacagg ctgcaggtga tgctctcca	120
ccttacagca gcatttctgc agagagcgca gcataatttg actacaagga tgagtctggg	180
tttccaaagc ccccatctta caatgtagct acaacactgc ccagttatga tgaagcggag	240
aggaccaagg ctgaagctac tatccctttg gttcctggga gagatgagga ttttgtgggt	300
cgggatgatt ttgatgatgc tgaccagctg aggataggaa atgatgggat ttcatgtta	360
acttttttca tggcattcct cttaactgg attgggtttt tctgtcttt ttgcctgacc	420
acttcagctg caggaaggta tggggccatt tcaggatttg gtctctctct aattaaatgg	480
atcctgattg tcaggttttc cacctatttc cctggatatt ttgatgtca gtactggctc	540
tggtgggtgt tctttgtttt aggctttctc ctgtttctca gaggatttat caattatgca	600
aaagttcgga agatgccaga aactttctca aatctcccca ggaccagagt tctctttatt	660
tat	663

278/307

<210> 141

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78)... (1091)

<400> 141

ctcttccccg gcccgcccg gcgggaccag tgcgcagccg gggctggcgg gcggcggggt	60
ccgcgggggcc gcaggag atg acg gcc ggc ggc cag gcc gag gcc gag ggc	110
Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly	
1 5 10	
gct ggc ggg gag ccc ggc gcg gcg cgg ctg ccc tcg cgg gtg gcc cgg	158
Ala Gly Gly Glu Pro Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg	
15 20 25	
ctg ctg tcg gcg ctc ttc tac ggg acc tgc tcc ttc ctc atc gtg ctt	206
Leu Leu Ser Ala Leu Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu	
30 35 40	
gtc aac aag gcg ctg ctg acc acc tac ggt ttc ccg tca cca att ttc	254
Val Asn Lys Ala Leu Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe	
45 50 55	
ctt gga att gga cag atg gca gcc acc ata atg ata cta tat gtg tcc	302
Leu Gly Ile Gly Gln Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser	
60 65 70 75	
aag cta aac aaa atc att cac ttc cct gat ttt gat aag aaa att cct	350

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Lys	Leu	Asn	Lys	Ile	Ile	His	Phe	Pro	Asp	Phe	Asp	Lys	Lys	Ile	Pro			
				80					85					90				
gta	aag	ctg	ttt	cct	ctg	cct	ctc	ctc	tac	gtt	gga	aac	cac	ata	agt	398		
Val	Lys	Leu	Phe	Pro	Leu	Pro	Leu	Leu	Tyr	Val	Gly	Asn	His	Ile	Ser			
				95					100					105				
gga	tta	tca	agc	aca	agt	aaa	tta	agc	cta	ccg	atg	ttc	acc	gtg	ctc	446		
Gly	Leu	Ser	Ser	Thr	Ser	Lys	Leu	Ser	Leu	Pro	Met	Phe	Thr	Val	Leu			
				110					115					120				
agg	aaa	ttc	acc	att	cca	ctt	acc	tta	ctt	ctg	gaa	acc	atc	ata	ctt	494		
Arg	Lys	Phe	Thr	Ile	Pro	Leu	Thr	Leu	Leu	Leu	Glu	Thr	Ile	Ile	Leu			
				125					130					135				
ggg	aag	cag	tat	tca	ctc	aac	atc	atc	ctc	agt	gtc	ttt	gcc	att	att	542		
Gly	Lys	Gln	Tyr	Ser	Leu	Asn	Ile	Ile	Leu	Ser	Val	Phe	Ala	Ile	Ile			
				140					145					150				
ctc	ggg	gct	ttc	ata	gca	gct	ggg	tct	gac	ctt	gct	ttt	aac	tta	gaa	590		
Leu	Gly	Ala	Phe	Ile	Ala	Ala	Gly	Ser	Asp	Leu	Ala	Phe	Asn	Leu	Glu			
				160					165					170				
ggc	tat	att	ttt	gta	ttc	ctg	aat	gat	atc	ttc	aca	gca	gca	aat	gga	638		
Gly	Tyr	Ile	Phe	Val	Phe	Leu	Asn	Asp	Ile	Phe	Thr	Ala	Ala	Asn	Gly			
				175					180					185				
gtt	tat	acc	aaa	cag	aaa	atg	gac	cca	aag	gag	cta	ggg	aaa	tac	gga	686		
Val	Tyr	Thr	Lys	Gln	Lys	Met	Asp	Pro	Lys	Glu	Leu	Gly	Lys	Tyr	Gly			
				190					195					200				
gta	ctt	ttc	tac	aat	gcc	tgc	ttc	atg	att	atc	cca	act	ctt	att	att	734		
Val	Leu	Phe	Tyr	Asn	Ala	Cys	Phe	Met	Ile	Ile	Pro	Thr	Leu	Ile	Ile			

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205	210	215	
agt gtc tcc act gga gac ctg caa cag gct act gaa ttc aac caa tgg			782
Ser Val Ser Thr Gly Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp			
220	225	230	235
aag aat gtt gtg ttt atc cta cag ttt ctt ctt tcc tgt ttt ttg ggg			830
Lys Asn Val Val Phe Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly			
	240	245	250
ttt ctg ctg atg tac tcc acg gtt ctg tgc agc tat tac aat tca gcc			878
Phe Leu Leu Met Tyr Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala			
	255	260	265
ctg acg aca gca gtg gtt gga gcc atc aag aat gta tcc gtt gcc tac			926
Leu Thr Thr Ala Val Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr			
	270	275	280
att ggg ata tta atc ggt gga gac tac att ttc tct ttg tta aac ttt			974
Ile Gly Ile Leu Ile Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe			
	285	290	295
gta ggg tta aat att tgc atg gca ggg ggc ttg aga tat tcc ttt tta			1022
Val Gly Leu Asn Ile Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu			
	300	305	310
aca ctg agc agc cag tta aaa cct aaa cct gtg ggt gaa gaa aac atc			1070
Thr Leu Ser Ser Gln Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile			
	320	325	330
tgt ttg gat ttg aag agc ta aagagtctgc agcaggattg gagactgact			1120
Cys Leu Asp Leu Lys Ser			

335

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tgtgactgcg ggctgggggg gcattcccag taggaatgtg aagccagagg tttcggattc 1180
 gtgacatcca ccccttgggc aagtgagagc atctgcaaaa tgcaaagaga actacctcat 1240
 atgcaggatg agccaatggc agtctcaaga aatgtactcg ggcgacacct tacctgtgga 1300
 aagcaaatct tttcaaaata agccactggg actcggtagg tggagcccca gctgctcttc 1360
 tagggaccta tggggccttc gtggcatctc tgtgctgtgt gctggggagg aggttgatgt 1420
 aatggtgact cttttctgat cagcaccttg gccgtgattc ccaaggtccc agccaaagca 1480
 aagggccagt tgtttcagtt taaacagaca tgtctttagt ctaataaaat tagttaactg 1540
 ccagtaaagt tatttgttag ctttgatgaa agctatgttg gtatctttcc ctaatcatca 1600
 aagtaaataa aaaatcattt ct 1622

<210> 142

<211> 2475

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)... (746)

<400> 142

acctgtggga gcgacccggg agaaggaggg ccaag atg gcg gaa gcg gag gag 53
 Met Ala Glu Ala Glu Glu
 1 5
 tct cca gga gac ccg ggg aca gca tcg ccc agg ccc ctg ttt gca ggc 101
 Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro Arg Pro Leu Phe Ala Gly
 10 15 20
 ctt tca gat ata tcc atc tca caa gac atc ccc gta gaa gga gaa atc 149

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Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile Pro Val Glu Gly Glu Ile
 25 30 35
 acc att cct atg aga tct cgc atc cgg gag ttt gac agc tcc aca tta 197
 Thr Ile Pro Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu
 40 45 50
 aat gaa tct gtt cgc aat acc atc atg cgt gat cta aaa gct gtt ggg 245
 Asn Glu Ser Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly
 55 60 65 70
 aaa aaa ttc atg cat gtt ttg tac cca agg aaa agt aat act ctt ttg 293
 Lys Lys Phe Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu
 75 80 85
 aga gat tgg gat ttg tgg ggc cct ttg atc ctt tgt gtg aca ctc gca 341
 Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala
 90 95 100
 tta atg ctg caa aga gac tct gca gat agt gaa aaa gat gga ggg ccc 389
 Leu Met Leu Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro
 105 110 115
 caa ttt gca gag gtg ttt gtc att gtc tgg ttt ggt gca gtt acc atc 437
 Gln Phe Ala Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile
 120 125 130
 acc ctc aac tca aaa ctt ctt gga ggg aac ata tct ttt ttt cag agc 485
 Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser
 135 140 145 150
 ctc tgt gtg ctg ggt tac tgt ata ctt ccc ttg aca gta gca atg ctg 533
 Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu

283/307

155	160	165	
att tgc cgg ctg gta ctt ttg gct gat cca gga cct gta aac ttc atg			581
Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met			
170	175	180	
gtt cgg ctt ttt gtg gtg att gtg atg ttt gcc tgg tct ata gtt gcc			629
Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala			
185	190	195	
tcc aca gct ttc ctt gct gat agc cag cct cca aac cgc aga gcc cta			677
Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu			
200	205	210	
gct gtt tat cct gtt ttc ctg ttt tac ttt gtc atc agt tgg atg att			725
Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile			
215	220	225	230
ctc acc ttt act cct cag taaatca ggaatgggaa attaaaaacc agtgaattga			780
Leu Thr Phe Thr Pro Gln			
235			
aagcacatct gaaagatgca attcaccatg gagctttgtc tctggccctt atttgtctaa			840
ttttggaggt atttgataac tgagtaggtg aggagattaa aaggagacca tatagcactg			900
tcacccctta tttaggaac tgatgtttga aaggctgttc ttttctctct taatgtcatt			960
tctttaaaaa tacatgtgca tactacacac agtatataat gcctccttaa ggcatgatgg			1020
agtcaccgtg gtccatttgg gtgacaacca gtgacttggg aagcacatag atacatctta			1080
caagttgaat agagttgata actatittca gttttgagaa taccagttca ggtgcagctc			1140
ttaaacacat tgccttatga ctattagaat atgcctctct tttcataaat aaaaatacat			1200
ggtctatata cattttcttt tatttctctc tcttaagctt aaaaaggcaa tgagagaggt			1260
taggagtggg ttcatacacg gagaatgaga aaacatgcat taaccaatat tcagattttg			1320

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atcaggggaa attctacact tgttgcaaaa aaaaaaaaaa aaaaagcaaa gggcctctaa 1380
 agaatcagcc tctttggtcc ctttgtctg tcacctttt gccatgttta acagcatctt 1440
 ggttggcact ctagtcttaa tctgtctct taactttgaa tatgcagtct aaaatgtcag 1500
 tagtcaacat gtaattttcc tttgaaattc tgaatattcc agtgctggaa cttatccaaa 1560
 aagaagacct cagaaactta gattggtaga tctctagtgc atattatcat gtgggcacct 1620
 tctcttaggg tggaatgagg cagtctggat gcagcatagt taaaaggagc tgtttaatat 1680
 tctctgtagt ctggcctctt aactagaaag taaagctaaa tcagaagcct gtatttaacc 1740
 atgtgaacag ggagggattt agtgttctga tggttgatta atagaacagc tagatactta 1800
 gagcatgacg tgggatggga tgagtttaca gctgctgcct tttcatggtg agcttagcag 1860
 ttttctcatt agatgtgttt ttttgggttg gggaatagca atttatttta ttgattttag 1920
 actttatcaa gctaattagc tcccccttag ataagtacat gttgcacatg tgcacctact 1980
 tgtaatctca gatatttatg cacacaagtg tgaaggtttt tcaggaggca gagcatctgg 2040
 gacaggctga ttctgagcta aacagggtc ctttaaggca atatgaactg ttgccttcta 2100
 taaattgcac attgaggaac tctaatagac aaagattagg tgtcaggcag aaaacactca 2160
 ttgtaaatat actattagtt gataaacata ggactttctt attccccagt ttttctttat 2220
 catataattt aaatatttat tcattttgta tttaaagact acctacacat agatatatga 2280
 ttccaaagtc atactttctc catccccaca ttagccaagt gaatacaggg ccaaattgggt 2340
 tcttggaatg ataataacaa agcattacaa agtgggtccc cttggttcca gccttgtcca 2400
 gagtttttgg ttatatattt ctatttatta caatttacct tttaaattgt aaaataaacc 2460
 tttgtgtgga cagag 2475

<210> 143

<211> 1739

<212> DNA

<213> Homo sapiens

285/307

<220>

<221> CDS

<222> (21)... (1703)

<400> 143

tgcgccctga cagcccaaca atg gcg gcg ccc gcg gag tcg ctg agg agg 50

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg

1 5 10

cgg aag act ggg tac tcg gat ccg gag cct gag tcg ccg ccc gcg ccg 98

Arg Lys Thr Gly Tyr Ser Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro

15 20 25

ggg cgt ggc ccc gca ggc tct ccg gcc cat ctc cac acg ggc acc ttc 146

Gly Arg Gly Pro Ala Gly Ser Pro Ala His Leu His Thr Gly Thr Phe

30 35 40

tgg ctg acc cgg atc gtg ctc ctg aag gcc cta gcc ttc gtg tac ttc 194

Trp Leu Thr Arg Ile Val Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe

45 50 55

gtg gca ttc ctg gtg gct ttc cat cag aac aag cag ctc atc ggt gac 242

Val Ala Phe Leu Val Ala Phe His Gln Asn Lys Gln Leu Ile Gly Asp

60 65 70

agg ggg ctg ctt ccc tgc aga gtg ttc ctg aag aac ttc cag cag tac 290

Arg Gly Leu Leu Pro Cys Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr

75 80 85 90

ttc cag gac agg acg agc tgg gaa gtc ttc agc tac atg ccc acc atc 338

Phe Gln Asp Arg Thr Ser Trp Glu Val Phe Ser Tyr Met Pro Thr Ile

95 100 105

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ctc tgg ctg atg gac tgg tca gac atg aac tcc aac ctg gac ttg ctg	386
Leu Trp Leu Met Asp Trp Ser Asp Met Asn Ser Asn Leu Asp Leu Leu	
110 115 120	
gct ctt ctc gga ctg ggc atc tcg tct ttc gta ctg atc acg ggc tgc	434
Ala Leu Leu Gly Leu Gly Ile Ser Ser Phe Val Leu Ile Thr Gly Cys	
125 130 135	
gcc aac atg ctt ctc atg gct gcc ctg tgg ggc ctc tac atg tcc ctg	482
Ala Asn Met Leu Leu Met Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu	
140 145 150	
gtt aat gtg ggc cat gtc tgg tac tct ttc gga tgg gag tcc cag ctt	530
Val Asn Val Gly His Val Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu	
155 160 165 170	
ctg gag acg ggg ttc ctg ggg atc ttc ctg tgc cct ctg tgg acg ctg	578
Leu Glu Thr Gly Phe Leu Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu	
175 180 185	
tca agg ctg ccc cag cat acc ccc aca tcc cgg att gtc ctg tgg ggc	626
Ser Arg Leu Pro Gln His Thr Pro Thr Ser Arg Ile Val Leu Trp Gly	
190 195 200	
ttc cgg tgg ctg atc ttc agg atc atg ctt gga gca ggc ctg atc aag	674
Phe Arg Trp Leu Ile Phe Arg Ile Met Leu Gly Ala Gly Leu Ile Lys	
205 210 215	
atc cgg ggg gac cgg tgc tgg cga gac ctc acc tgc atg gac ttc cac	722
Ile Arg Gly Asp Arg Cys Trp Arg Asp Leu Thr Cys Met Asp Phe His	
220 225 230	
tat gag acc cag ccg atg ccc aat cct gtg gca tac tac ctg cac cac	770

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Tyr Glu Thr Gln Pro Met Pro Asn Pro Val Ala Tyr Tyr Leu His His
 235 240 245 250
 tca ccc tgg tgg ttc cat cgc ttc gag acg ctc agc aac cac ttc atc 818
 Ser Pro Trp Trp Phe His Arg Phe Glu Thr Leu Ser Asn His Phe Ile
 255 260 265
 gag ctc ctg gtg ccc ttc ttc ctc ttc ctc ggc cgg cgg gcg tgc atc 866
 Glu Leu Leu Val Pro Phe Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile
 270 275 280
 atc cac ggg gtg ctg cag atc ctg ttc cag gcc gtc ctc atc gtc agc 914
 Ile His Gly Val Leu Gln Ile Leu Phe Gln Ala Val Leu Ile Val Ser
 285 290 295
 ggg aac ctc agc ttc ctg aac tgg ctg act atg gtg ccc agc ctg gcc 962
 Gly Asn Leu Ser Phe Leu Asn Trp Leu Thr Met Val Pro Ser Leu Ala
 300 305 310
 tgc ttt gat gac gcc acc ctg gga ttc ttg ttc ccc tct ggg cca gcc 1010
 Cys Phe Asp Asp Ala Thr Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly
 315 320 325 330
 agc ctg aag gac cga gtt ctg cag atg cag agg gac atc cga ggg gcc 1058
 Ser Leu Lys Asp Arg Val Leu Gln Met Gln Arg Asp Ile Arg Gly Ala
 335 340 345
 cgg ccc gag ccc aga ttc ggc tcc gtg gtg cgg cgt gca gcc aac gtc 1106
 Arg Pro Glu Pro Arg Phe Gly Ser Val Val Arg Arg Ala Ala Asn Val
 350 355 360
 tcg ctg ggc gtc ctg ctg gcc tgg ctc agc gtg ccc gtg gtc ctc aac 1154
 Ser Leu Gly Val Leu Leu Ala Trp Leu Ser Val Pro Val Val Leu Asn

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365	370	375	
ttg ctg agc tcc agg cag gtc atg aac acc cac ttc aac tct ctt cac			1202
Leu Leu Ser Ser Arg Gln Val Met Asn Thr His Phe Asn Ser Leu His			
380	385	390	
atc gtc aac act tac ggg gcc ttc gga agc atc acc aag gag cgg gcg			1250
Ile Val Asn Thr Tyr Gly Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala			
395	400	405	410
gag gtg atc ctg cag ggc aca gcc agc tcc aac gcc agc gcc ccc gat			1298
Glu Val Ile Leu Gln Gly Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp			
415	420	425	
gcc atg tgg gag gac tac gag ttc aag tgc aag cca ggt gac ccc agc			1346
Ala Met Trp Glu Asp Tyr Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser			
430	435	440	
aga cgg ccc tgc ctc atc tcc ccg tac cac tac cgc ctg gac tgg ctg			1394
Arg Arg Pro Cys Leu Ile Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu			
445	450	455	
atg tgg ttc gcg gcc ttc cag acc tac gag cac aac gac tgg atc atc			1442
Met Trp Phe Ala Ala Phe Gln Thr Tyr Glu His Asn Asp Trp Ile Ile			
460	465	470	
cac ctg gct ggc aag ctc ctg gcc agc gac gcc gag gcc ttg tcc ctg			1490
His Leu Ala Gly Lys Leu Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu			
475	480	485	490
ctg gca cac aac ccc ttc gcg ggc agg ccc ccg ccc agg tgg gtc cga			1538
Leu Ala His Asn Pro Phe Ala Gly Arg Pro Pro Pro Arg Trp Val Arg			
495	500	505	

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gga gag cac tac agg tac aag ttc agc cgt cct ggg ggc agg cac gcc 1586

Gly Glu His Tyr Arg Tyr Lys Phe Ser Arg Pro Gly Gly Arg His Ala

510

515

520

gcc gag ggc aag tgg tgg gtg cgg aag agg atc gga gcc tac ttc cct 1634

Ala Glu Gly Lys Trp Trp Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro

525

530

535

ccg ctc agc ctg gag gag ctg agg ccc tac ttc agg gac cgt ggg tgg 1682

Pro Leu Ser Leu Glu Glu Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp

540

545

550

cct ctg ccc ggg ccc ctc tagacgtgca ccagaaataa aggccaagac 1730

Pro Leu Pro Gly Pro Leu

555

560

ccagccccc

1739

<210> 144

<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107)... (1327)

<400> 144

ggagcccagc ggccgggtgtg agagtccgta aggagcagct tccaggatcc tgagatccgg 60

agcagccggg gtcggagcgg ctctcaaga gttactgac tatgaa atg gca gag 115

Met Ala Glu

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1

aat gga aaa aat tgt gac cag aga cgt gta gca atg aac aag gaa cat	163
Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn Lys Glu His	
5 10 15	
cat aat gga aat ttc aca gac ccc tct tca gtg aat gaa aag aag agg	211
His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg	
20 25 30 35	
agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag ccg ctc	259
Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu	
40 45 50	
att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg aag gaa	307
Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu	
55 60 65	
tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct ttt tta	355
Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu	
70 75 80	
ctg ctg ctt gct gtg ctt ata gct acg tat tat gtt gaa gga gtg cat	403
Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His	
85 90 95	
caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat gcc tac	451
Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr	
100 105 110 115	
tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca ggg ctg	499
Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu	
120 125 130	

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cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt aca tta	547
His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu	
135 140 145	
gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc tat cct	595
Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro	
150 155 160	
gat cag att att tgt cca gat gaa gag ggc act gaa gga acc att tct	643
Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser	
165 170 175	
ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg tgg ggt	691
Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly	
180 185 190 195	
atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc aga gca	739
Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala	
200 205 210	
gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag gaa ttt	787
Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe	
215 220 225	
gaa gag atg ctg gaa cat gca gag tct gca caa gac ttt gcc tcc cgg	835
Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe Ala Ser Arg	
230 235 240	
gcc aaa ctg gca gtt caa aaa cta gta cag aaa gtt gga ttt ttt gga	883
Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly Phe Phe Gly	
245 250 255	
att ttg gcc tgt gct tca att cca aat cct tta ttt gat ctg gct gga	931

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Ile	Leu	Ala	Cys	Ala	Ser	Ile	Pro	Asn	Pro	Leu	Phe	Asp	Leu	Ala	Gly		
260					265					270					275		
ata	acg	tgt	gga	cac	ttt	ctg	gta	cct	ttt	tgg	acc	ttc	ttt	ggt	gca	979	
Ile	Thr	Cys	Gly	His	Phe	Leu	Val	Pro	Phe	Trp	Thr	Phe	Phe	Gly	Ala		
					280					285					290		
acc	cta	att	gga	aaa	gca	ata	ata	aaa	atg	cat	atc	cag	aaa	att	ttt	1027	
Thr	Leu	Ile	Gly	Lys	Ala	Ile	Ile	Lys	Met	His	Ile	Gln	Lys	Ile	Phe		
					295					300					305		
gtt	ata	ata	aca	ttc	agc	aag	cac	ata	gtg	gag	caa	atg	gtg	gct	ttc	1075	
Val	Ile	Ile	Thr	Phe	Ser	Lys	His	Ile	Val	Glu	Gln	Met	Val	Ala	Phe		
					310					315					320		
att	ggt	gct	gtc	ccc	ggc	ata	ggt	cca	tct	ctg	cag	aag	cca	ttt	cag	1123	
Ile	Gly	Ala	Val	Pro	Gly	Ile	Gly	Pro	Ser	Leu	Gln	Lys	Pro	Phe	Gln		
					325					330					335		
gag	tac	ctg	gag	gct	caa	cgg	cag	aag	ctt	cac	cac	aaa	agc	gaa	atg	1171	
Glu	Tyr	Leu	Glu	Ala	Gln	Arg	Gln	Lys	Leu	His	His	Lys	Ser	Glu	Met		
					340					345					350		
ggc	aca	cca	cag	gga	gaa	aac	tgg	ttg	tcc	tgg	atg	ttt	gaa	aag	ttg	1219	
Gly	Thr	Pro	Gln	Gly	Glu	Asn	Trp	Leu	Ser	Trp	Met	Phe	Glu	Lys	Leu		
					360					365					370		
gtc	gtt	gtc	atg	gtg	tgt	tac	ttc	atc	cta	tct	atc	att	aac	tcc	atg	1267	
Val	Val	Val	Met	Val	Cys	Tyr	Phe	Ile	Leu	Ser	Ile	Ile	Asn	Ser	Met		
					375					380					385		
gca	caa	agt	tat	gcc	aaa	cga	atc	cag	cag	cgg	ttg	aac	tca	gag	gag	1315	
Ala	Gln	Ser	Tyr	Ala	Lys	Arg	Ile	Gln	Gln	Arg	Leu	Asn	Ser	Glu	Glu		

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390	395	400	
aaa act aaa taagta gagaaagttt taaactgcag aaattggagt ggatgggttc			1370
Lys Thr Lys			
405			
tgccittaaat tgggaggact ccaagccggg aaggaaaatt cccttttcca acctgtatca			1430
atttttacaa cttttttcct gaaagcagtt tagtccatac ttigcactga catacttttt			1490
ccttcigtgc taaggttaagg tateccacct cgatgcaatc caccttgtgt tttcttaggg			1550
tggaatgtga tggtcagcag caaacttgca acagactggc ctctgtttg ttactttcaa			1610
aaggcccaca tgatacaatt agagaattcc caccgcacaa aaaaagttcc taagtatgtt			1670
aaatatgtca agcttttttag gcttgtcaca aatgattgct ttgttttcct aagtcacaa			1730
aatgtatata aattatctag attggataac agtcttgcac gtttatcatg ttacaattta			1790
atattccatc ctgcccaacc cttcctctcc catcctcaaa aaagggccat tttatgatgc			1850
attgcacacc ctctggggaa attgatcttt aaattttgag acagtataag gaaaatctgg			1910
ttggtgtctt acaagtgagc tgacaccatt ttttattctg tgtatttaga atgaagtctt			1970
gaaaaaaact ttataaagac atctttaatc attcc			2005

<210> 145

<211> 1558

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (31)... (1392)

<400> 145

tcccggtcgg gtgcaaggag ccgaggcgag atg ggc gtc ctg ggc cgg gtc ctg	54
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294/307

Met Gly Val Leu Gly Arg Val Leu

1

5

ctg tgg ctg cag ctc tgc gca ctg acc cag gcg gtc tcc aaa ctc tgg 102

Leu Trp Leu Gln Leu Cys Ala Leu Thr Gln Ala Val Ser Lys Leu Trp

10

15

20

gtc ccc aac acg gac ttc gac gtc gca gcc aac tgg agc cag aac cgg 150

Val Pro Asn Thr Asp Phe Asp Val Ala Ala Asn Trp Ser Gln Asn Arg

25

30

35

40

acc ccg tgc gcc ggc ggc gcc gtt gag ttc ccg gcg gac aag atg gtg 198

Thr Pro Cys Ala Gly Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val

45

50

55

tca gtc ctg gtg caa gaa ggt cac gcc gtc tca gac atg ctc ctg ccg 246

Ser Val Leu Val Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro

60

65

70

ctg gat ggg gaa ctc gtc ctg gct tca gga gcc gga ttc ggc gtc tca 294

Leu Asp Gly Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser

75

80

85

gac gtg ggc tcg cac ctg gac tgt ggc gcg ggc gaa cct gcc gtc ttc 342

Asp Val Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe

90

95

100

cgc gac tct gac cgc ttc tcc tgg cat gac ccg cac ctg tgg cgc tct 390

Arg Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser

105

110

115

120

ggg gac gag gca cct ggc ctc ttc ttc gtg gac gcc gag cgc gtg ccc 438

Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val Pro

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125	130	135	
tgc cgc cac gac gac gtc ttc ttt ccg cct agt gcc tcc ttc cgc gtg			486
Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe Arg Val			
140	145	150	
ggg ctc ggc cct ggc gct agc ccc gtg cgt gtc cgc agc atc tcg gct			534
Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser Ile Ser Ala			
155	160	165	
ctg ggc cgg acg ttc acg cgc gac gag gac ctg gct gtt ttc ctg gcg			582
Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala Val Phe Leu Ala			
170	175	180	
tcc cgc gcg ggc cgc cta cgc ttc cac ggg ccg ggc gcg ctg agc gtg			630
Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro Gly Ala Leu Ser Val			
185	190	195	200
ggc ccc gag gac tgc gcg gac ccg tcg ggc tgc gtc tgc ggc aac gcg			678
Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly Cys Val Cys Gly Asn Ala			
205	210	215	
gag gcg cag ccg tgg atc tgc gcg gcc ctg ctc cag ccc ctg ggc ggc			726
Glu Ala Gln Pro Trp Ile Cys Ala Ala Leu Leu Gln Pro Leu Gly Gly			
220	225	230	
cgc tgc ccc cag gcc gcc tgc cac agc gcc ctc cgg ccc cag ggg cag			774
Arg Cys Pro Gln Ala Ala Cys His Ser Ala Leu Arg Pro Gln Gly Gln			
235	240	245	
tgc tgt gac ctc tgt gga gcc gtt gtg ttg ctg acc cac ggc ccc gca			822
Cys Cys Asp Leu Cys Gly Ala Val Val Leu Leu Thr His Gly Pro Ala			
250	255	260	

296/307

ttt gac ctg gag cgg tac cgg gcg cgg ata ctg gac acc ttc ctg ggt	870
Phe Asp Leu Glu Arg Tyr Arg Ala Arg Ile Leu Asp Thr Phe Leu Gly	
265 270 275 280	
ctg cct cag tac cac ggg ctg cag gtg gcc gtg tcc aag gtg cca cgc	918
Leu Pro Gln Tyr His Gly Leu Gln Val Ala Val Ser Lys Val Pro Arg	
285 290 295	
tcg tcc cgg ctc cgt gag gcc gat acg gag atc cag gtg gtg ctg gtg	966
Ser Ser Arg Leu Arg Glu Ala Asp Thr Glu Ile Gln Val Val Leu Val	
300 305 310	
gag aat ggg ccc gag aca ggc gga gcg ggg cgg ctg gcc cgg gcc ctc	1014
Glu Asn Gly Pro Glu Thr Gly Gly Ala Gly Arg Leu Ala Arg Ala Leu	
315 320 325	
ctg gcg gac gtc gcc gag aac ggc gag gcc ctc ggc gtc ctg gag gcg	1062
Leu Ala Asp Val Ala Glu Asn Gly Glu Ala Leu Gly Val Leu Glu Ala	
330 335 340	
acc atg cgg gag tcg ggc gca cac gtc tgg ggc agc tcc gcg gct ggg	1110
Thr Met Arg Glu Ser Gly Ala His Val Trp Gly Ser Ser Ala Ala Gly	
345 350 355 360	
ctg gcg ggc ggc gtg gcg gct gcc gtg ctg ctg gcg ctg ctg gtc ctg	1158
Leu Ala Gly Gly Val Ala Ala Ala Val Leu Leu Ala Leu Leu Val Leu	
365 370 375	
ctg gtg gcg ccg ccg ctg ctg cgc cgc gcg ggg agg ctc agg tgg agg	1206
Leu Val Ala Pro Pro Leu Leu Arg Arg Ala Gly Arg Leu Arg Trp Arg	
380 385 390	
agg cac gag gcg gcg gcc ccg gct gga gcg ccc ctc ggc ttc cgc aac	1254

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Arg His Glu Ala Ala Ala Pro Ala Gly Ala Pro Leu Gly Phe Arg Asn
 395 400 405
 ccg gtg ttc gac gtg acg gcc tcc gag gag ctg ccc ctg ccg cgg cgg 1302
 Pro Val Phe Asp Val Thr Ala Ser Glu Glu Leu Pro Leu Pro Arg Arg
 410 415 420
 ctc agc ctg gtt ccg aag gcg gcc gca gac agc acc agc cac agt tac 1350
 Leu Ser Leu Val Pro Lys Ala Ala Ala Asp Ser Thr Ser His Ser Tyr
 425 430 435 440
 ttc gtc aac cct ctg ttc gcc ggg gcc gag gcc gag gcc t gagcggccgc 1400
 Phe Val Asn Pro Leu Phe Ala Gly Ala Glu Ala Glu Ala
 445 450
 ctgaccgtcg accttggggc tctccacccc ctctggcccc agtcgaactg ggggctagcc 1460
 acctctctgt ccagccccca aacctcccct tcctttcccc ctctctccggg ggccaaggac 1520
 aggggtggcct tactcagtaa aggtgtttcc tgcacctg 1558

<210> 146

<211> 1005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)... (330)

<400> 146

attcctgtaa tggctgcttc ctagaaggtc gtgtcacgtg gaacctctta atctcagcat 60
 ccggagctcc aggaaggga aatttcaagt cagatagaat tctatatata ccatttcttt 120

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ggaaccttca gccctcaaga ttccaacatc atg acc tca gtt tca aca cag ttg 174
 Met Thr.Ser Val Ser Thr Gln Leu
 1 5
 tcc tta gtc ctc atg tca ctg ctt ttg gtg ctg cct gtt gtg gaa gca 222
 Ser Leu Val Leu Met Ser Leu Leu Leu Val Leu Pro Val Val Glu Ala
 10 15 20
 gta gaa gcc ggt gat gca atc gcc ctt ttg tta ggt gtg gtt ctc agc 270
 Val Glu Ala Gly Asp Ala Ile Ala Leu Leu Leu Gly Val Val Leu Ser
 25 30 35 40
 att aca ggc att tgt gcc tgc ttg ggg gta tat gca cga aaa aga aat 318
 Ile Thr Gly Ile Cys Ala Cys Leu Gly Val Tyr Ala Arg Lys Arg Asn
 45 50 55
 gga cag atg tga ctttgaaagg cctactgagt caaacctcac cctgaaaacc 370
 Gly Gln Met
 tttgcgcttt agaggctaaa cctgagattt ggtgtgtgaa aggttccaag aatcagtaaa 430
 taaggaggatt tcacattttt cattgtttcc atgaaatggc aacaaacata catttataaa 490
 ttgaaaaaaa aatgttttct ttacaacaaa taatgcacag aaaaatgcag cctataattt 550
 gctagttagg tagtcaaaga agtaagatgg ctgaaattta cataagtaat atttcataat 610
 cttagaattc tctcaaagca tgtgaaatag gaagaaggaa gttcttgccc agaatcttag 670
 gaaatcacca ctgttcggtt ataactactg cctcctgaat cgttgaggag tcttttaaatt 730
 tagatttttg ttttgtgtc tccaagtta atattatatt tagatatcag agagtcaggc 790
 aaaaaggaaa acttttatct ctagggaaaa aacatttaga aaaatgtatt cagtgtatct 850
 aatactgaaa tgcggaaaaa aatttaatgt taataaaaaa actatagaca ttgacatgga 910
 aaagagattt aatgttttga aaaaaaactt tatattaact gagtaacatc ctctgatga 970
 gaagtactat attaaatata aaccattat gttat 1005

299/307

<210> 147

<211> 969

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)... (783)

<400> 147

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ggtcgctcag ccctgccgtc cttcaccacc acaccttcac ctgcgccag ctccctgcgc 120

gcctggacag cgctgtctgc ccgcctcccg atg gcc ctg ccc cag atg tgt gac 174

Met Ala Leu Pro Gln Met Cys Asp

1

5

ggg agc cac ttg gcc tcc acc ctc cgc tat tgc atg aca gtc agc ggc 222

Gly Ser His Leu Ala Ser Thr Leu Arg Tyr Cys Met Thr Val Ser Gly

10

15

20

aca gtg gtt ctg gtg gcc ggg acg ctc tgc ttc gct tgg tgg agc gaa 270

Thr Val Val Leu Val Ala Gly Thr Leu Cys Phe Ala Trp Trp Ser Glu

25

30

35

40

ggg gat gca acc gcc cag cct ggc cag ctg gcc cca ccc acg gag tat 318

Gly Asp Ala Thr Ala Gln Pro Gly Gln Leu Ala Pro Pro Thr Glu Tyr

45

50

55

ccg gtg cct gag ggc ccc agc ccc ctg ctc agg tcc gtc agc ttc gtc 366

Pro Val Pro Glu Gly Pro Ser Pro Leu Leu Arg Ser Val Ser Phe Val

300/307

60	65	70	
tgc tgc ggt gca ggt ggc ctg ctg ctg ctc att ggc ctg ctg tgg tcc			414
Cys Cys Gly Ala Gly Gly Leu Leu Leu Leu Ile Gly Leu Leu Trp Ser			
75	80	85	
gtc aag gcc agc atc cca ggg cca cct cga tgg gac ccc tat cac ctc			462
Val Lys Ala Ser Ile Pro Gly Pro Pro Arg Trp Asp Pro Tyr His Leu			
90	95	100	
tcc aga gac ctg tac tac ctc act gtg gag tcc tca gag aag gag agc			510
Ser Arg Asp Leu Tyr Tyr Leu Thr Val Glu Ser Ser Glu Lys Glu Ser			
105	110	115	120
tgc agg acc ccc aaa gtg gtt gac atc ccc act tac gag gaa gcc gtg			558
Cys Arg Thr Pro Lys Val Val Asp Ile Pro Thr Tyr Glu Glu Ala Val			
125	130	135	
agc ttc cca gtg gcc gag ggg ccc cca aca cca cct gca tac cct acg			606
Ser Phe Pro Val Ala Glu Gly Pro Pro Thr Pro Pro Ala Tyr Pro Thr			
140	145	150	
gag gaa gcc ctg gag cca agt gga tcg agg gat gcc ctg ctc agc acc			654
Glu Glu Ala Leu Glu Pro Ser Gly Ser Arg Asp Ala Leu Leu Ser Thr			
155	160	165	
cag ccc gcc tgg cct cca ccc agc tat gag agc atc agc ctt gct ctt			702
Gln Pro Ala Trp Pro Pro Pro Ser Tyr Glu Ser Ile Ser Leu Ala Leu			
170	175	180	
gat gcc gtt tct gca gag acg aca ccg agt gcc aca cgc tcc tgc tca			750
Asp Ala Val Ser Ala Glu Thr Thr Pro Ser Ala Thr Arg Ser Cys Ser			
185	190	195	200

301/307

ggc ctg gtt cag act gca cgg gga gga agt taaaggctcc tagcaggtcc 800

Gly Leu Val Gln Thr Ala Arg Gly Gly Ser

205

210

tgaatccaga gacaaaaatg ctgtgccttc tccagagtct tatgcagtgc ctgggacaca 860

gtaggcactc agcaaacgtt cggtgttgaa ggctgttcta tttatctatt gctgtataac 920

aaaccacccc agaatttagt ggcttaaaat aaatccatt ttattatgt 969

<210> 148

<211> 1241

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)... (517)

<400> 148

atttcggggc ggtaccaag atg gac tcc tcg cgg gcc cga cag cag ctc cgg 52

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg

1

5

10

cgg cga ttc ctc ctc ctg ccg gac gcc gag gcc cag ctg gac cgc gag 100

Arg Arg Phe Leu Leu Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu

15

20

25

ggc gac gcc ggg ccg gaa acc tcc aca gct gtt gag aaa aag gag aaa 148

Gly Asp Ala Gly Pro Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys

30

35

40

cct ctt cca aga ctt aat atc cat tct gga ttc tgg att ttg gca tcc 196

302/307

Pro Leu Pro Arg Leu Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser
 45 50 55
 att gtt gtg acc tat tat gtt gac ttc ttt aaa acc ctt aaa gaa aac 244
 Ile Val Val Thr Tyr Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn
 60 65 70 75
 ttc cac act agc agc tgg ttt ctc tgt ggc agt gcc ttg ttg ctt gtc 292
 Phe His Thr Ser Ser Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val
 80 85 90
 agt tta tca att gca ttt tac tgc ata gtc tac ctg gaa tgg tat tgt 340
 Ser Leu Ser Ile Ala Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys
 95 100 105
 gga att gga gaa tat gat gtc aag tat cca gcc ttg ata ccc att acc 388
 Gly Ile Gly Glu Tyr Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr
 110 115 120
 act gcc tcc ttt att gca gca gga att tgc ttc aac att gct tta tgg 436
 Thr Ala Ser Phe Ile Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp
 125 130 135
 cat gtg tgg tcg ttt ttc act cca ttg ttg ttg ttt acc cag ttt atg 484
 His Val Trp Ser Phe Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met
 140 145 150 155
 ggg gtt gtc atg ttt atc aca ctc ctt gga tgattt ccgaagagac 530
 Gly Val Val Met Phe Ile Thr Leu Leu Gly
 160 165
 aggggtcttct atgttgccca ggetgtcttt gaactcctgg gatcaagtga tcctcctgcc 590
 tcagccttcg aagtagttgg gactacaggc ccagccacc gtgcctggct ggacatgtaa 650

303/307

atttgaagtg aatggttaaa catccagcta gctgaaagca tggcagaccc taacagaaaa 710
 gctacagtgt gtttttcag ctatgaagtg aatggtttcc tggggaaaat tgtgactttg 770
 tataactgtt gttgaaacca gaataaatta tatttcactt gcatatgcat aaattattaa 830
 aattttcaga agtcagtgat acagaagtac tattttgcaa tgttaatctg tttgagtctt 890
 tggagaaagt ggtttcattg taggtacata gtgcactgtt aatattttta acaagtagtt 950
 cactcttcca ttttaaggat agcagttcct tgtataaaat gactggatgt gtataaagga 1010
 attatgttgt catgtgcctt taaccagctt tagtaattac tataatctca tatttatgat 1070
 agttttgtta ggtgacagga ccaaagaaa atattttatg ttttctcatc actttagatt 1130
 ttatcattat gtacattact gggtttttag catttcctaa tgtgaagttt taatcacttt 1190
 taagtataca ttttttctg tatcatttaa ataaaatatt tttataactt t 1241

<210> 149

<211> 1174

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (187)... (675)

<400> 149

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Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln

1

5

10

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ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc tca gaa ctg	276
Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu	
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ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc atc cag gat	324
Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp	
35 40 45	
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Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn	
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acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc cat aag ttc	420
Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe	
65 70 75	
aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc agc atc tcc	468
Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser	
80 85 90	
ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc aac agc ttc	516
Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe	
95 100 105 110	
ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag aga cta gca	564
Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala	
115 120 125	
gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta aga cta ggc	612
Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly	
130 135 140	
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Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met

145

150

155

caa gtt cga agg tgacctct tgtcacactg atggatactt ttccttcctg 710

Gln Val Arg Arg

160

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cggcctccca gcgtcccaa gccgcagcgg ccgcgccct tcagctagct cgctcgctcg 180

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ctctgcttcc ctgctgccgg ctgcgcc atg gcg ttg gcg ttg gcg gcg ctg	231
Met Ala Leu Ala Leu Ala Ala Leu	
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Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn	
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gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct cca	327
Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro	
25 30 35 40	
cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac aag	375
Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr Lys	
45 50 55	
gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca aca	423
Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr Thr	
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Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile	
75 80 85	
cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat ttt	519
Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe	
90 95 100	
gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg tta	567
Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu	
105 110 115 120	
act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg tct	615

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Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser
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 Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly
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 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr
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 Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe
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 Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala
 185 190 195 200
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 Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg
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 Val Leu Phe Ile Tyr
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